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Parent selection to maximize heterosis expression in soybean (Glycine max L. [Merr.])

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Parent selection to maximize heterosis expression in soybean (*Glycine max* L. [Merr.])

by

Francisco Jonathan Cerna

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TABLE OF CONTENTS

INTRODUCTION

Utilization of heterosis effects in breeding soybean [Glycine max (L.) Merr] cultivars for commercial production is still a possibility. Heterotic effects in soybean for yield and other economic traits have been reported (Chauhan and Singh, 1982; Mehta et al., 1984; Nelson and Bernard, 1984; Paschal and Wilcox, 1975; and Raut et al., 1988). Parents of these populations were selected on the basis of differences for morphological characteristics, for yielding ability, and for geographic origin. Not all hybrid combinations, however, were heterotic for yield and for some of the other traits considered. One interpretation for these results is that the criteria used in selecting the parents may not provide accurate means to estimate genetic diversity in soybean.

Parents could also be selected on the basis of differences in molecular markers such as restriction fragment length polymorphisms and isozyme constitution. These markers express loci differences among genotypes (Lander and Botstein, 1989; Tanksley, 1983). They therefore, could be used as criteria to select parents for hybrid combinations if an association is found between heterosis and markers as a measure of genetic diversity. There are no published reports in soybean in which the relationship between genetic diversity at the molecular level and heterosis expression has been studied. One objective of this research was to determine heterosis expression in soybean germplasms obtained from the crossing of parents selected on the basis of restriction fragment length polymorphism (RFLP) diversity and isozyme loci (ISO) constitution compared

to parents selected for high-yielding (HY) ability and differences in geographic origin (GO).

Heterosis expression in soybean has been evaluated in the F_1 generation (Chaudhary and Singh, 1974; Chauhan and Singh, 1982; Leffel and Weiss, 1958; Mehta et al., 1984; Nelson and Bernard, 1984; Paschal and Wilcox, 1975; Raut et al., 1988; Srivastava et al., 1978; Veatch, 1930; Weber et al., 1970; Weiss et al., 1947). The F_1 generation allows for the maximum expression of heterosis (Falconer, 1981). In soybean because of the difficulties in obtaining by artificial hybridization the large numbers of F_1 seed that will be required to conduct replicated tests, the F_1 evaluations have been conducted on a single-plant basis (Chaudhary and Singh, 1974; Chauhan and Singh, 1982; Leffel and Weiss, 1958; Mehta et al., 1984; Paschal and Wilcox, 1975; Raut et al., 1988; Srivastava et al., 1978; Veatch, 1930; Weber et al., 1970; Weiss et al., 1947). The F_1 generation could be evaluated in replicated tests using the hill plot technique (Garland and Fehr, 1981), because few seeds are needed to plant each hill. The evaluation at the F_2 generation may be conducted in larger plots and in replicated experiments because seed supply usually is not limiting. A generation of seed increase would be necessary to plant these experiments. Selfing to the F_2 may break down the genetic combinations that show heterotic effects. The reliability of these estimates will depend on the association between heterotic effects expressed in the F_1 and the F_2 generations. In soybean there are no published reports in which the heterosis expression of F_1 hybrid combinations has been compared to the expression in the F_2 generation. The second objective of this research was

to compare mean heterotic performance of F_1 hybrids and F_2 bulks evaluated in hill- and row-plots to determine the association between heterosis expression in both generations.

LITERATURE REVIEW

Hybrid cultivars are used for the commercial production of numerous plant species (Hayes and Foster, 1976). The phenomenon of heterosis has been generally associated with increased yield and vigor obtained by crossing highly selected inbred lines of cross-pollinating crops. With the realization of the possibility of producing F_1 hybrids on a large scale, increasing attention has been given to heterosis in self-pollinating crops. The major considerations in hybrid production for a breeder of agriculturally important self-pollinating crops are, first, whether or not it is possible to obtain sufficient heterosis for characters of economic importance under conditions which also give high yields per unit area of land, and, secondly, whether or not it is possible to fix such heterosis in pure breeding lines (Hayes and Foster, 1976).

Most of the detailed genetic information regarding the expression of heterosis in self-pollinating crops has come from diallel crosses of selected parents with the evaluation of F_1 hybrids, ocassionally of F_2 populations, and more rarely of subsequent generations (Hayes and Foster, 1976). The expression of heterosis has been associated with the interaction of different alleles at a locus (Castle, 1946; Falconer, 1981; Gustafson, 1947; Hallauer and Miranda, 1988; Hull, 1945; Jones, 1945).

The theoretical expression of heterosis is measured by comparing the F_1 hybrid performance with the midparent value (Falconer, 1981). The useful expression of heterosis, on the other hand, is measured by comparing the F_1 hybrid performance with the higher parent. In soybean, heterosis has been

measured by comparing F_1 hybrid performance to midparent and high-parent values (Chaudhary and Singh, 1974; Nelson and Bernard, 1984; Paschal and Wilcox, 1975; Raut et al., 1988; Srivastava et al., 1978; Veatch, 1930; Weber et al., 1970; Weiss et al., 1947). Evaluations at the F_2 and subsequent generations have not been conducted with the objective to measure heterosis expression, but rather to estimate genetic variability (Chauhan and Singh, 1982), to compare individual transgressive segregates at the F_2 generation with individual hybrid plants at the F_1 generation (Veatch, 1930), to predict the outcome of a large number of crosses in early generation trials (Weiss et al., 1947), and to estimate inbreeding depression (Mehta et al., 1984). In soybean, no reports have been published in which the heterosis expression of F_1 hybrid combinations has been compared to the expression in the F_2 generation.

Heterosis estimates for yield

Observations on hybrid soybeans occurred early in the modern history of soybean breeding (Veatch, 1930; Wentz and Stewart, 1924). Early research on heterosis revealed superiority of the F_1 hybrids over the higher parent for yield and plant height characteristics (Veatch, 1930; Weiss et al., 1947; Woodworth, 1933). In a study involving 17 F_1 hybrids, Weiss et al. (1947) reported average high-parent heterosis for seed yield of 14% in field tests and 32% in greenhouse tests. Leffel and Weiss (1958), in a 10-parent diallel found that of 45 hybrids, 14 showed significant high-parent heterosis for yield. The average midparent heterosis for yield was 13.7%. Weber et al. (1970) evaluated 85 different F_1 hybrids during 4 years. The midparent and high-parent heterosis for yield averaged 25% and 13.4%,

respectively.

In general, the mean high-parent heterotic response for yield of hybrid soybeans reported in the literature have ranged from 8% (Paschal and Wilcox, 1975) to 26% (Chaudhary and Singh, 1974) with most between 13 and 20% (Brim and Cockerham, 1961; Kalton, 1948; Veatch, 1930; Weber et al., 1970; Weiss et al., 1947). More important for hybrid cultivar development are the highest values of high-parent heterosis reported, which have ranged from 17% (Paschal and Wilcox, 1975) to 90% (Weber et al., 1970).

Heterosis for traits other than yield

The relationship between yield and yield components of soybean hybrids has been determined. Anand and Torrie (1963) in a study involving three different soybean crosses, found that number of pods per plant and number of seed per pod were more closely associated phenotypically with high seed yield than seed size. According to Weber et al. (1970), seed size could not be responsible for yield heterosis in soybean hybrids, because hybrids had smaller seeds than their respective higher yielding parent. The authors suggested that seed number was the component responsible for yield heterosis.

Raut et al. (1988) observed maximum positive heterosis values for individual F_1 hybrids over the better parent in primary branches per plant (81.75%), pods per plant (96.91%), and seeds per plant (110.24%). Critical evaluation of their data revealed heterosis for yield to be due to the hybrid vigor present in the yield component traits, suggesting that pods and seeds per plant had made the maximum contribution to total seed yield. These findings are in conformity with earlier reports by Weber et al.

(1970) and Rao et al. (1978).

Small heterotic effects have been observed for harvest index (Paschal and Wilcox, 1975; Weber et al., 1970), seed weight (Chaudhary and Singh, 1974; Leffel and Weiss, 1958; Paschal and Wilcox, 1975; Veatch, 1930; Weber et al., 1970), and number of seeds per pods (Chaudhary and Singh, 1974; Paschal and Wilcox, 1975; Veatch, 1930). Heterotic effects for the number of pods per plant have been greater than for any other trait measured except yield (Chaudhary and Singh, 1974; Paschal and Wilcox, 1975; Veatch, 1930). Heterosis for the number of pods per plant and for yield, however, were often not observed in the same hybrid combination (Chaudhary and Singh, 1974; Raut et al., 1988).

Some researchers have observed that a small percentage of the hybrids are significantly taller than the taller parent (Chaudhary and Singh, 1974; Leffel and Weiss, 1958; Woodworth, 1933). Others however, point out that plant height of the hybrid is intermediate between the midparent value and the height of the taller parent (Brim and Cockerham, 1961; Kalton, 1948; Paschal and Wilcox, 1975; Veatch, 1930; Weber et al., 1970). Date of flowering and date of maturity of hybrid soybeans also were generally intermediate between the midparent value and the later flowering and maturing parent (Brim and Cockerham, 1961; Chaudhary and Singh, 1974; Leffel and Weiss, 1958; Weber et al., 1970; Weiss et al., 1947). Small, mostly nonsignificant heterotic effects have been found for protein and oil content (Nelson and Bernard, 1984; Weber et al., 1970) and also for plant lodging (Nelson and Bernard, 1984; Paschal and Wilcox, 1975).

Genetic diversity and heterosis

The use of exotic or widely diverse germplasm in breeding programs has been studied in many crop species as it relates with heterosis expression. Moll et al. (1965) state that genetic differences between corn (Zea mays L.) cultivars have arisen through geographic isolation accompanied by a combination of genetic drift and selection in different environments. In a study of corn cultivars from three geographic regions, the authors observed that the greater the diversity in geographic origin of the parental open-pollinated cultivars, the higher yielding was the cross. This finding suggests that crosses of widely diverged parents may have potential use in yield improvement even if the parents crossed are not adapted to the local conditions.

Niehaus and Pickett (1966) and Malm (1968) conducted experiments using adapted sorghum [Sorghum bicolor (L.) Moench] cultivars and plant introductions from Africa. Findings of both studies indicated that genetic diversity was the key to obtain hybrid vigor, because the crosses involving geographically diverse and presumably genetically diverse parents produced the highest yielding hybrids. The same relationship between geographical diversity of parents and heterosis of their hybrid combinations has been reported in peanuts (Arachis hypogaea L.) by Parker et al.(1970); in tobacco (Nicotiana tabacum L.) by Vandenberg and Matzinger (1970); and in tall fescue (Festuca arundinacea Schreb.) by Matzinger and Frakes (1973).

In soybean, previous studies have directed efforts to evaluate heterosis in populations formed using parents that have been selected on the basis of differences for morphological characteristics, yielding

ability, and geographic origin (Chaudhary and Singh, 1974; Mehta et al., 1984; Nelson and Bernard, 1984; Paschal and Wilcox, 1975; Raut et al., 1988). Paschal and Wilcox (1975) evaluated 10 hybrid combinations of different parental origins. Parents included adapted cultivars and plant introductions from both the same and different geographic origin. All of the 10 hybrid combinations produced hybrids that at least outyielded the midparent value. The adapted x adapted and chinese x chinese combinations significantly outyielded the high-parent values. Although none of the parental combinations showed significant heterosis for number of seeds per pod on either the midparent or the high-parent basis, six combinations were significantly ($P<0.05$) different from the midparent value for the number of pods per plant. Two of the parental combinations, adapted x korean and korean x korean, showed midparent heterosis for seed size. None of the combinations produced hybrids that differed significantly from the midparent or the high-parent in maturity. Adapted x adapted, adapted x chinese, and chinese x chinese crosses were significantly taller than their respective midparent values; and the chinese x chinese hybrids were more lodging-prone than the midparent. Heterosis for plant weight (air-dry weight in g of aerial portion of plant before threshing) followed the same pattern than yield, with the adapted x adapted and chinese x chinese combinations showing midparent heterosis. No significant heterosis was noted for harvest index. Diversity of geographic origin has been a key to obtain hybrid vigor (Moll et al., 1965; Niehaus and Pickett, 1966; Malm, 1968). This was not evident in the study by Paschal and Wilcox (1975).

Chauhan and Singh (1982) reported on a study conducted to determine the relationship between genetic diversity, measured from Mahalanobis D^2 values, and heterosis in the F_1 and the genetic variance estimated in the F_2 generation of populations of soybean. The selected parents represented cultivars with different levels of divergence as measured by Mahalanobis D^2 values. On the basis of the magnitude of inter-cluster distances, varieties were grouped into highly divergent, moderately divergent, and less divergent classes. The data on heterosis indicated that with increase in divergence between parents there was an increase in heterosis up to a certain level considered the optimum level of divergence, beyond which the overall heterosis for yield is partly cancelled due to negative heterosis for certain yield components. In general, Chauhan and Singh (1982) observed that divergent crosses had high heterosis for most of the traits measured. Maximum heterosis however, was not observed in the most divergent crosses, this was displayed by crosses in which the parents were moderately diverse. For most of the characters, greater variability in the genetic variance of the F_2 was observed on the crosses between moderate to highly diverse parents. Similar results were obtained by Moll et al. (1965) in maize. Ramanujan et al. (1974) in mungbean (Phaseolus aureus Roxb.) observed an agreement between the extent of heterosis and the genetic divergence between the parents.

In soybean, it has been estimated that 12 ancestors contributed 88% of the germplasm collection of 136 U.S. and Canadian soybean cultivars of Maturity Group (MG) 00 to IV released between 1939 and 1981 (Specht and Williams, 1984). It is apparent then that the production of soybean hybrids

would be based on the crossing of high-yielding lines that are somewhat related. Nelson and Bernard (1984) studied heterosis in soybean by crossing high-yielding parents that were unselected for combining ability. The authors found low significant ($P<0.05$) heterosis for all traits measured, with the level of expression generally lower than previously reported. They found, however, significant yield heterosis in one hybrid combination involving two parents that were selected from the same cross. The authors concluded that differences between the pedigrees of the parents was not a requirement for heterosis. Weber et al. (1970), in a previous study evaluating hybrids by crossing high-yielding lines, also found significant ($P<0.05$) superiority of F_1 hybrids over the midparent and high-parent values. They did not report, however, any pedigree relationship between the parents of each cross. It appears, thus, that a certain level of coancestry may be acceptable for observing significant heterosis in crosses involving closely related parents.

Estimates of genetic similarity or distance between plants may be useful in planning crosses for hybrid or homozygous cultivar development. The coancestry coefficient (Malecot, 1948) between genotypes, as the Mahalanobis D^2 measure of genetic distance (Chauhan and Singh, 1982), has been widely used to estimate levels of genetic diversity between cultivars in autogamous crop species such as wheat (Triticum aestivum L.: Cox et al., 1985b; Murphy et al., 1986), oat (Avena sativa L.: Rodgers et al., 1983; Souza and Sorrells, 1989), and soybean (Cox et al., 1985a). A relationship between different levels of coancestry and heterosis, however, has not been studied in soybeans.

Molecular approaches to assess genetic diversity

Isozymes. Studies have been conducted to relate isozyme heterozygosity to heterosis expression in maize (Lamkey et al., 1987; Price et al., 1986). Price et al. (1986) collected field data on single-cross hybrids obtained from crossing 48 inbred lines. Genotypes of the crosses were determined from parental inbred genotypes at 13 polymorphic isozyme loci. The authors found cross performance to be unrelated to allelic differences among the inbred lines at the 13 isozyme loci studied. Lamkey et al. (1987) also studied the relationship between allelic differences at enzyme loci and cross performance in maize. Data collected at 11 isozyme loci on 24 high-yielding and 21 low-yielding lines indicated that allelic differences between lines were not predictive of hybrid performance.

One interesting potential use of isozymes in soybean research is the possibility of using markers to classify cultivars for maximum genetic distance (Kiang and Gorman, 1983). Using 12 polymorphic isozyme systems as markers and 100 named northern cultivars as samples, Kiang and Gorman (1983) ran a cluster analysis to estimate genetic distance among cultivars. The authors found that cultivars which had been used effectively as parents in crosses for cultivar development showed significantly greater genetic distance than shown by any two cultivars drawn at random. Cox et al. (1985a) estimated genetic similarity between two soybean cultivars released in the 1950s, 1960s, and 1970s on the basis of the coefficient of parentage and similarity indices based on a combination of loci differences for 7 morphological and 11 isozyme markers. They found rank correlation between the two estimates to be significantly ($P<0.01$) and positively associated,

although intermediate in magnitude, indicating that both estimates measure genetic relationship but give independent estimates. The data obtained by Cox et al. (1985a) showed a wide range of genetic similarity and distance among the soybean cultivars studied. This evidence suggests that genetic distance as calculated by isozyme loci may be a useful guide in selecting successful parents in a breeding program. There are no reports on the association between heterosis and isozyme diversity in soybean.

RFLPs. Burr et al. (1983) suggested the use of RFLPs for estimating genetic diversity, mapping genes that control quantitatively inherited traits, and selecting for increased heterozygosity or homozygosity. Several studies have been conducted in maize to determine the relationship of RFLP molecular markers with hybrid performance and heterosis (Dudley et al., 1991; Godshalk et al., 1990; Lee et al., 1989; Melchinger et al., 1990; Smith et al., 1990). In most studies using RFLPs in maize, the correlation of hybrid performance with molecular marker diversity between parents has been too low to be of any predictive value (Dudley et al., 1991; Godshalk et al., 1990; Lee et al., 1989; Melchinger et al., 1990). Smith et al. (1990) found, however, a high correlation between RFLP-based genetic distance and grain yield and grain yield heterosis at the F_1 generation, suggesting that measures of similarity as calculated from RFLP data could allow maize breeders to predict combinations of lines that will result in high-yielding single-cross hybrids. Most of the studies conducted to relate RFLP marker diversity with hybrid performance and heterosis in maize have, however, suggested that RFLP data can be used for assigning inbreds into heterotic groups but may not have predictive value for hybrid performance

(Godshalk et al., 1990; Lee et al., 1989; Melchinger et al., 1990; Melchinger et al., 1991; Smith et al., 1990).

In soybean, the identification of a large number of RFLP markers has progressed slowly compared to species such as maize and tomato, due in part to a lack of genetic variation in the germplasm and a lack of cytogenetic markers (Keim et al., 1990). Previous studies in Glycine max have identified low levels of restriction site polymorphism which prevented extensive genetic mapping (Apuya et al., 1988; Doyle, 1988; Doyle and Beachy, 1985). A survey of 58 wild and cultivated soybean accessions from the subgenus Soja, however, identified genetically diverse genotypes (Keim et al., 1989).

Markers identified by Keim et al. (1990) have been used to develop the latest published RFLP soybean genome map. Keim et al. (1990) reported a RFLP map of ca 1200 centimorgans, in contrast to the ca 530 centimorgans present in the previously reported map summarized by Palmer and Kilen (1987). Keim et al. (1990) used 150 RFLPs to identify linkages in an F_2 segregating population from an interspecific cross (Glycine max x Glycine soja). The identification of these large number of RFLP markers could provide more molecular information to estimate genetic distances among soybean genotypes. There are no available reports however, on the association between heterosis expression and RFLP diversity in soybean.

MATERIALS AND METHODS

Development and evaluation of genotypes

Twenty one genotypes of each of Maturity Groups (MG) II and III, selected according to four criteria: HY, and for differences in RFLP, ISO. and GO were used in crossing to obtain 24 F_1 hybrids and their F_2 bulks (Table 1). Six hybrid combinations were obtained within each selection criterion and MG (Table 2). Genotypes for the HY selection criterion were selected on the basis of high yield and were crossed in a partial diallel with no reciprocals. Parents for the RFLP group were selected and crossed according to their genetic distance as indicated by a principal component analysis (PCA) in a survey conducted by Keim et al. (1989). For the ISO group, parents were selected from a survey conducted by Griffin and Palmer (Unpublished data, 1986). The two genotypes selected for crossing differed at 6 isozyme loci. Genotypes from different geographic areas (USA, China, Korea, Japan, and Poland) were chosen and crossed for the GO selection criterion.

Twelve to 48 F_1 seeds for each hybrid combination were obtained at the Iowa State University-University of Puerto Rico research site in Isabela, Puerto Rico in May 1989. The F_1 seed was grown in Ames, IA during the summer of 1989 to obtain F_2 seed. Crosses were repeated during the same season to obtain a minimum of 48 more F_1 seeds. If additional F_1 or F_2 seed was needed for any of the combinations, this was obtained in the winter and spring of 1989-1990 at the site in Puerto Rico and in the summer of 1990 at Ames, IA. Flower, pubescence, and hilum color were used as markers to

Table 1. Genotypes of MG II and III per selection criterion used for crossing and information on the origin, pedigree, and originator

Criterion§	Genotype	Origin	Pedigree
		MG II ¶	
HY	Hack	USA	L70T-543G x K1028
	Elgin 87	USA	Elgin[5] x Williams 82
	Conrad	USA	A3127 x Tri-Valley Charger
	Kenwood	USA	Elgin x A1937
RFLP †	Corsoy(25)	USA	Harosoy x Capital
	Asgrow25AF(23)	USA	X1878 x X2717
	Seneca(42)	China	FC. 036554A
	Harosoy(29)	USA	Mandarin x A.K. (Harrow)
	Richland(37)	China	PI70.502-2
	A80-244036(21)	USA	A74-204034 x Cumberland
ISO	Magna	USA	[Mandarin x Jogun]x[Mandarin x Kanro]
	Mukden	China	PI50.523Q
	Funman	USA	Selection from Manchu
	Bansei	Japan	PI81.031
	Beeson 80	USA	Beeson[8] x Arksoy
GO	Tastee	USA-Japan	PI86.019
	PI30.594	Manchuria-China	Unknown
	PI69.501	China	Unknwon
	PI80.671	Japan	Unknown

† Number in parenthesis is the PCA number after Keim et al. (1989).
‡ AES= Agricultural experiment station.
§ HY= High yield; RFLP= Restriction fragment length polymorphism; ISO= Isozyme; GO= Geographic origin.
¶ MG II= Maturity Group II; MG III= Maturity Group III.

Originator	Reference
Illinois AES ‡	Nickell et al. (1985).
Iowa AES ‡	Fehr et al. (1988).
Iowa AES ‡	Fehr et al. (1989).
Iowa AES ‡	Cianzio et al. (1990).
Iowa AES ‡	Weber and Fehr (1970).
Asgrow Seed Company	Palmer et al. (1990).
R.G. Wiggans, New York AES‡ and USDA	Morse et al. (1949).
Department of Agriculture Experiment Station, Harrow, Canada	Weiss and Stevenson (1955).
Purdue AES ‡, Indiana, and USDA	Morse and Cartter (1939).
Iowa AES ‡	Not released.
Iowa AES ‡	Weber (1967).
Iowa AES ‡ and USDA	Morse and Cartter (1939).
Funk Brothers Seed Co., Illinois	Morse (1948).
USDA	Morse (1936).
Purdue AES ‡, Indiana and USDA	Wilcox et al. (1980).
USDA	Morse et al. (1949).
-	INTSOY (1987, Vol I)
-	INTSOY (1987, Vol I)
-	INTSOY (1987, Vol I)

Table 1. Continued

Criterion§	Genotype	Origin	Pedigree
		MG II ¶	
GO	PI84.580	Korea	Unknown
	Richland	USA-China	PI70.502-2
		MG III ¶	
HY	Zane	USA	Cumberland x Pella
	Resnik	USA	A3127 x Williams 82
	A86-801024	USA	A81-356022 x LN78-1136
	Sherman	USA	A72-512 x Pella
RFLP †	A81-356022(20)	USA	Century x A76-304020
	Illini(36)	China	Selection from A.K.
	Dunfield(41)	China	PI36.846
	PI437.477B(17)	USSR	Unknown
ISO	Cloud	China	PI16.790
	Cumberland	USA	Corsoy x Williams
	Will	USA	Williams^{6} x (Clark x T117)
	Williams 82	USA	Williams^{7} x Kingwa
	Mandell	USA	Selection from Manchu
	BSR 301	USA	L15 x AP68-1016
	Shelby	USA	Lincoln^{2} x Richland
GO	PI80.470	Japan	Unknown

Originator	Reference
-	INTSOY (1987, Vol I)
Purdue AES ‡, Indiana and USDA	Morse and Cartter (1939).
Ohio ARDC	Walker et al. (1986).
Ohio ARDC	McBlain et al. (1990).
Iowa AES ‡	Not released.
Ohio ARDC	McBlain et al. (1987).
Iowa AES ‡	Not released.
C.M. Woodworth, Illinois AES ‡	Morse (1927).
Purdue AES ‡, Indiana	Morse (1927).
-	INTSOY (1987, Vol I).
USDA	Piper and Morse (1910).
Iowa AES ‡ and Puerto Rico AES ‡	Bahrenfus and Fehr (1988).
Illinois AES ‡ and USDA	Bernard and Cremeens (1988b).
Illinois AES ‡ and USDA	Bernard and Cremeens (1988a).
G.H. Cutler, Purdue AES ‡, Indiana	Morse and Cartter (1939).
Iowa AES ‡ and USDA	Tachibana et al. (1980).
Illinois AES ‡	Johnson (1960).
-	INTSOY (1987, Vol I).

Table 1. Continued

Criterion§	Genotype	Origin	Pedigree
		MG III ¶	
GO	PI104.708	Poland	Unknown
	PI61.940	China	Unknown
	PI82.235	Korea	Unknown
	Manchuria	USA-China	PI28.050
	PI54.592	Manchuria	Unknown

Originator	Reference
-	INTSOY (1987, Vol I).
-	INTSOY (1987, Vol I).
-	INTSOY (1987, Vol I).
USDA	Piper and Morse (1923).
-	INTSOY (1987, Vol I).

Table 2. Parents of Maturity Group II and III per selection criterion and their hybrid combinations

Criterion‡	Genotype	Hybrid Combinations
	MG II§	
HY	1-Hack	2x1, 3x2, 4x3,
	2-Elgin 87	4x2, 1x4, 3x1
	3-Conrad	
	4-Kenwood	
RFLP †	5-Corsoy(25)	6x5, 5x10, 8x7
	6-Asgrow25AF(23)	7x6, 9x6, 10x9
	7-Seneca(42)	
	8-Harosoy(29)	
	9-Richland(37)	
	10-A80-244036(21)	
ISO	11-Magna	12x11, 13x12, 14x11
	12-Mukden	15x12, 15x13, 15x14
	13-Funman	
	14-Bansei	
	15-Beeson 80	
GO	16-Tastee	17x18, 17x16, 18x21
	17-PI30.594	19x20, 19x16, 19x21
	18-PI69.501	
	19-PI80.671	
	20-PI84.580	
	21-Richland	
	MG III§	
HY	22-Zane	23x22, 24x23, 25x24
	23-Resnik	25x23, 22x25, 24x22
	24-A86-801024	
	25-Sherman	
RFLP †	26-A81-356022(20)	29x26, 27x26, 26x28
	27-Illini(36)	28x27, 29x27, 29x28
	28-Dunfield(41)	
	29-PI437.477B(17)	

† Number in parenthesis is the PCA number after Keim et al. (1989).

‡ HY= High yield; RFLP= Restriction fragment length polymorphism; ISO= Isozyme; GO= Geographic origin.

§ MG II= Maturity group II; MG III= Maturity group III.

Table 2. (Continued)

Criterion‡	Genotype	Hybrid Combinations
	MG III§	
ISO	30-Cloud	31x30, 32x30, 35x30
	31-Cumberland	34x36, 33x30, 34x30
	32-Will	
	33-Williams 82	
	34-Mandell	
	35-BSR 301	
	36-Shelby	
GO	37-PI80.470	38x37, 41x40, 39x42
	38-PI104.708	42x40, 39x37, 40x37
	39-PI61.940	
	40-PI82.235	
	41-Manchuria	
	42-PI54.592	

confirm F_1 hybrid plants that were harvested in bulk. For the combinations in which no such markers were available, the F_1 plants were harvested individually. The identity of these populations was maintained until the planting of the F_2 seed at which time observations of segregation for plant height and maturity date were used to confirm the hybrid nature of these populations.

For each MG, the 21 parents, the 24 F_1 hybrids and their F_2 bulks for the four selection criteria were evaluated in hill- and row-plot experiments planted on 30 May 1990 and 29 May 1991. The experiments were conducted at two locations each year at the Iowa State University Agronomy and Agricultural Engineering Research Center near Ames, IA. The soil type at the Ames and Burkey locations is a clarion loam.

The hill-plot experiment included the parents, the F_1 hybrids and their F_2 bulks planted twice in each replication for a total of 69 entries. Plots consisted of single, unbordered hills spaced 102 x 102 cm planted with twelve seeds in a linear distance of about 15 cm. Plots were not thinned (Garland and Fehr, 1981). Hills with fewer than three plants were considered as missing plots. Seeds of the cultivar Kenwood, MG II, and of Resnik, MG III, were planted in these plots before the adjacent hills had one fully developed trifoliolate leaf.

The row-plot experiment included the parents and the F_2 bulks for a total of 45 entries. The row plots consisted of two unbordered rows with 69 cm between rows within the plot and 102 cm between plots (Fehr, 1978; Gedge et al., 1977). Rows were 4.6 m long planted with 26 seeds m^{-1}. The center 3.1 m of both rows was harvested for yield.

Data was collected on an individual plot basis for seed yield, and agronomic and seed traits, described below:

1. Seed yield (YLD): weight of seed artificially dried at 38° C for 72 hours, expressed in g m^{-2}.

Agronomic traits:

2. Days to flowering (FLW): days after June 30 of first flower at any of the four uppermost nodes (R2, Fehr and Caviness, 1977).
3. Days to physiological maturity (MAT): days after August 31 when 95% of the pods reached their mature color (R8, Fehr and Caviness, 1977).
4. Lodging score (LDG): visual rating from 1, all plants erect, to 5, all plants prostrate at maturity.
5. Plant height (HT): distance from the soil surface to the terminal node with a pod at maturity, expressed in cm.

Seed traits:

6. One hundred-seed weight (SDWT): weight of 200 seeds divided by two, expressed in gr 100^{-1} seeds.
7 Protein (PROT) content: percentage of protein in a seed sample of 10 g, expressed as g kg^{-1} on a moisture-free basis.
8. Oil (OIL) content: percentage of oil in a seed sample of 10 g, expressed as g kg^{-1} on a moisture-free basis.

The protein and oil analyses were conducted in a near-infrared analyzer by the USA Northern Regional Research Center, Peoria, IL.

Mid-parent (MPH) and high-parent (HPH) heterosis for the F_1 and F_2 generations were calculated for every trait of each hybrid combination using the following equations:

F_1 MPH = F_1 - MP F_1 HPH = F_1 - HP

F_2 MPH = F_2 - MP F_2 HPH = F_2 - HP

where MP= midparent value, and HP= high-parent value. Values were expressed in the same units as described for each trait measured.

Statistical analyses

A randomized complete-block design with two replications at each location was used for the hill and row plot experiments in 1990 and 1991 for each MG. The data for each trait were analyzed for individual years over locations (Table 3) and then combined over environments (year-location combinations) (Table 4). In the mixed model of the analysis of variance (ANOVA), replications, locations, and environments were random effects and selection criteria and genotypes (parents, F_1 hybrids, F_2 bulks) were fixed effects. The ANOVA was performed using PROC ANOVA in SAS (SAS User's Guide: Statistics, Version 5 Edition, 1985).

For the analysis of individual years over locations, the following model was used:

$$Y_{ijk} = \mu + B_i + R_{j(i)} + E_k + (BE)_{ik} + e_{ijk}$$

where:

Y_{ijk}= observed value of the kth entry in the jth replication at the ith location;

μ= overall mean;

B_i= effect of the ith location, i= 1 to 2;

$R_{j(i)}$= effect of the jth replication in the ith location, j= 1 to 2;

E_k= effect of the kth entry, k= 1 to 69 in hill plot experiment and 1 to 45 in row plot experiment.

Table 3. Analysis of variance combined over locations for individual years for the hill- and row-plot experiments

Source	df †	Mean Squares	Expected Mean Squares
Locations (B)	(b-1)		$\sigma^2 + e\sigma^2_{r/b} + re\sigma^2_b$
Replications/B (R/B)	b(r-1)		$\sigma^2 + e\sigma^2_{r/b}$
Entries (E)	(e-1)	MS_{18}	$\sigma^2 + r\sigma^2_{be} + rb\theta^2_e$
Among Criteria (C)	(c-1)	MS_{17}	$\sigma^2_{r/bc} + r\sigma^2_{bc} + rb\theta^2_c$
Entries within C1 (E1)	(e1-1)	MS_{16}	$\sigma^2_{r/be1} + r\sigma^2_{be1} + rb\theta^2_{e1}$
Entries within C2 (E2)	(e2-1)	MS_{15}	$\sigma^2_{r/be2} + r\sigma^2_{be2} + rb\theta^2_{e2}$
Entries within C3 (E3)	(e3-1)	MS_{14}	$\sigma^2_{r/be3} + r\sigma^2_{be3} + rb\theta^2_{e3}$
Entries within C4 (E4)	(e4-1)	MS_{13}	$\sigma^2_{r/be4} + r\sigma^2_{be4} + rb\theta^2_{e4}$
B x E	(b-1)(e-1)	MS_{12}	$\sigma^2 + r\sigma^2_{be}$
BxC	(b-1)(c-1)	MS_{11}	$\sigma^2_{r/bc} + r\sigma^2_{bc}$
BxE1	(b-1)(e1-1)	MS_{10}	$\sigma^2_{r/be1} + r\sigma^2_{be1}$
BxE2	(b-1)(e2-1)	MS_9	$\sigma^2_{r/be2} + r\sigma^2_{be2}$
BxE3	(b-1)(e3-1)	MS_8	$\sigma^2_{r/be3} + r\sigma^2_{be3}$
BxE4	(b-1)(e4-1)	MS_7	$\sigma^2_{r/be4} + r\sigma^2_{be4}$
Error	b(r-1)(e-1)	MS_6	σ^2
R/BC	b(r-1)(c-1)	MS_5	$\sigma^2_{r/bc}$
R/BE1	b(r-1)(e1-1)	MS_4	$\sigma^2_{r/be1}$
R/BE2	b(r-1)(e2-1)	MS_3	$\sigma^2_{r/be2}$
R/BE3	b(r-1)(e3-1)	MS_2	$\sigma^2_{r/be3}$
R/BE4	b(r-1)(e4-1)	MS_1	$\sigma^2_{r/be4}$

† df= Degrees of freedom.

Table 4. Analysis of variance combined over environments for the hill and row plot experiments

Source	df †	Mean Squares	Expected Mean Squares
Environments (A)	(a-1)		$\sigma^2 + e\sigma^2_{r/a} + re\sigma^2_a$
Replications/A (R/A)	a(r-1)		$\sigma^2 + e\sigma^2_{r/a}$
Entries (E)	(e-1)	MS_{18}	$\sigma^2 + r\sigma^2_{ae} + ra\theta^2_e$
Among Criteria (C)	(c-1)	MS_{17}	$\sigma^2_{r/ac} + r\sigma^2_{ac} + ra\theta^2_c$
Entries within C1 (E1)	(e1-1)	MS_{16}	$\sigma^2_{r/ae1} + r\sigma^2_{ae1} + ra\theta^2_{e1}$
Entries within C2 (E2)	(e2-1)	MS_{15}	$\sigma^2_{r/ae2} + r\sigma^2_{ae2} + ra\theta^2_{e2}$
Entries within C3 (E3)	(e3-1)	MS_{14}	$\sigma^2_{r/ae3} + r\sigma^2_{ae3} + ra\theta^2_{e3}$
Entries within C4 (E4)	(e4-1)	MS_{13}	$\sigma^2_{r/ae4} + r\sigma^2_{ae4} + ra\theta^2_{e4}$
A x E	(a-1)(e-1)	MS_{12}	$\sigma^2 + r\sigma^2_{ae}$
AxC	(a-1)(c-1)	MS_{11}	$\sigma^2_{r/ac} + r\sigma^2_{ac}$
AxE1	(a-1)(e1-1)	MS_{10}	$\sigma^2_{r/ae1} + r\sigma^2_{ae1}$
AxE2	(a-1)(e2-1)	MS_9	$\sigma^2_{r/ae2} + r\sigma^2_{ae2}$
AxE3	(a-1)(e3-1)	MS_8	$\sigma^2_{r/ae3} + r\sigma^2_{ae3}$
AxE4	(a-1)(e4-1)	MS_7	$\sigma^2_{r/ae4} + r\sigma^2_{ae4}$
Error	a(r-1)(e-1)	MS_6	σ^2
R/AC	a(r-1)(c-1)	MS_5	$\sigma^2_{r/ac}$
R/AE1	a(r-1)(e1-1)	MS_4	$\sigma^2_{r/ae1}$
R/AE2	a(r-1)(e2-1)	MS_3	$\sigma^2_{r/ae2}$
R/AE3	a(r-1)(e3-1)	MS_2	$\sigma^2_{r/ae3}$
R/AE4	a(r-1)(e4-1)	MS_1	$\sigma^2_{r/ae4}$

† df= Degrees of freedom.

$(BE)_{ik}$= effect of the interaction of the ith location with the kth entry;

e_{ijk}= random error associated with the ijk observation.

The mean square due to entries in each analysis of variance was subdivided into variation among criteria (C1=HY, C2=RFLP, C3=ISO, and C4=GO) and variation among entries within selection criteria [HY (E1), RFLP (E2), ISO (E3), GO(E4)] (Table 3). The significance of entries was tested against the location x entry mean square. Entries within selection criteria were tested against their respective location x entry mean square. Single-degree of freedom comparison contrasts were calculated to detect significant differences between the mean performance of the F_1 hybrids or F_2 bulks and the MP value and among generations within each selection criterion. A LSD estimate was used to test significant differences between the mean performance of each F_1 hybrid or F_2 bulk and its respective high parent (HP):

$$LSD = t_{df,0.05}\sqrt{2\frac{MSE}{N}}$$

where:

t= tabular Student's value for the 0.05 level of probability and the degrees of freedom for the error term;

MSE= Mean square of the location x entry interaction;

N= the number of observations in the mean.

A combined analysis of variance over environments was conducted for the 1990 and 1991 data (Table 4). The following model over environments was used:

$$Y_{ijk} = \mu + A_i + R_{j(i)} + E_k + (AE)_{ik} + e_{ijk}$$

where:

Y_{ijk}= observed value of the kth entry in the jth replication at the ith environment;

μ= overall mean;

A_i= effect of the ith environment, i= 1 to 4;

$R_{j(i)}$= effect of the jth replication in the ith environment; j= 1 to 2;

E_k= effect of the kth entry; k= 1 to 69 in hill plot experiment and 1 to 45 in row plot experiment.

$(AE)_{ik}$= effect of the interaction of the ith environment with the kth entry;

e_{ijk}= random error associated with the ijk observation.

The entry mean squares of the analysis of variance over environments (Table 4) were subdivided similarly as for the analysis of variance over locations (Table 3). The significance of entries was tested against the environment x entry mean squares (Table 4). Entries within each selection criterion were tested against their respective environment x entry mean squares. Significant differences between the F_1 hybrids or F_2 bulks and the midparent or high-parent values were detected as described for the analysis of variance combined over locations for every individual year, using the environment x entry mean square as the error term.

A combined analysis of variance over years and locations was also conducted (Table 5). Years, locations, and replications were considered random effects and selection criteria and genotypes fixed effects. The following model was used:

$$Y_{ijkl} = \mu + Y_i + L_j + YL_{ij} + R_{k(ij)} + E_l + YE_{il} + LE_{jl} + YLE_{ijl} + e_{ijkl};$$

where:

Y_{ijkl}= observed value of the lth entry in the kth replication at the jth location and ith year.

μ= overall mean;

Y_i= effect of the ith year, i= 1 to 2;

L_j= effect of the jth location, j= 1 to 2;

YL_{ij}= effect of the interaction of the ith year with jth location;

$R_{k(ij)}$= effect of the kth replication in the ith year and jth location, k= 1 to 2;

E_l= effect of the lth entry, l= 1 to 69 in hill plot experiment and 1 to 45 in row plot experiment;

YE_{il}= effect of the interaction of the ith year with the lth entry;

LE_{jl}= effect of the interaction of the jth location with the lth entry;

YLE_{ijl}= effect of the interaction of the ith year with the jth location with the lth entry;

e_{ijkl}= random error associated with the ijkl observation;

The entry mean square (Table 5) was subdivided as described previously (Tables 3 and 4). The significance of entries was tested using

Table 5. Analysis of variance combined over years and locations for the hill and row plot experiments

Source	df †	Mean Squares	Expected Mean Squares
Years (Y)	(y-1)		$\sigma^2 + \sigma^2_{r(yl)} + r\sigma^2_{yl} + lr\sigma^2_{y}$
Locations (L)	(l-1)		$\sigma^2 + \sigma^2_{r(yl)} + r\sigma^2_{yl} + yr\sigma^2_{l}$
Y x L	(y-1)(l-1)		$\sigma^2 + \sigma^2_{r(yl)} + r\sigma^2_{yl}$
Replications/Y/L (R/Y/L)	yl(r-1)		$\sigma^2 + \sigma^2_{r(yl)}$
Entries (E)	(e-1)	MS_{30}	$\sigma^2 + r\sigma^2_{ylc} + ry\sigma^2_{lc} + rl\sigma^2_{yc} + ylr\Theta^2_{e}$
Among Criteria (C)	(c-1)	MS_{29}	$\sigma^2_{r(ylc)} + r\sigma^2_{ylc} + ry\sigma^2_{lc} + rl\sigma^2_{yc} + ylr\Theta^2_{c}$
Entries within C1 (E1)	(e1-1)	MS_{28}	$\sigma^2_{r(yle1)} + r\sigma^2_{yle1} + ry\sigma^2_{le1} + rl\sigma^2_{ye1} + ylr\Theta^2_{e1}$
Entries within C2 (E2)	(e2-1)	MS_{27}	$\sigma^2_{r(yle2)} + r\sigma^2_{yle2} + ry\sigma^2_{le2} + rl\sigma^2_{ye2} + ylr\Theta^2_{e2}$
Entries within C3 (E3)	(e3-1)	MS_{26}	$\sigma^2_{r(yle3)} + r\sigma^2_{yle3} + ry\sigma^2_{le3} + rl\sigma^2_{ye3} + ylr\Theta^2_{e3}$
Entries within C4 (E4)	(e4-1)	MS_{25}	$\sigma^2_{r(yle4)} + r\sigma^2_{yle4} + ry\sigma^2_{le4} + rl\sigma^2_{ye4} + ylr\Theta^2_{e4}$
Y x E	(y-1)(e-1)	MS_{24}	$\sigma^2 + r\sigma^2_{ylc} + lr\sigma^2_{yc}$
YxC	(y-1)(c-1)	MS_{23}	$\sigma^2_{r(ylc)} + r\sigma^2_{ylc} + lr\sigma^2_{yc}$
YxE1	(y-1)(e1-1)	MS_{22}	$\sigma^2_{r(yle1)} + r\sigma^2_{yle1} + lr\sigma^2_{ye1}$

† df= Degrees of freedom.

Table 5. Continued

Source	df †	Mean Squares	Expected Mean Squares
YxE2	(y-1)(e2-1)	MS_{21}	$\sigma^2_{r(yle2)} + r\sigma^2_{(yle2)} + lr\sigma^2_{(ye2)}$
YxE3	(y-1)(e3-1)	MS_{20}	$\sigma^2_{r(yle3)} + r\sigma^2_{(yle3)} + lr\sigma^2_{(ye3)}$
YxE4	(y-1)(e4-1)	MS_{19}	$\sigma^2_{r(yle4)} + r\sigma^2_{(yle4)} + lr\sigma^2_{(ye4)}$
L x E	(l-1)(e-1)	MS_{18}	$\sigma^2 + r\sigma^2_{(yle)} + yr\sigma^2_{(le)}$
LxC	(l-1)(c-1)	MS_{17}	$\sigma^2_{r(yle)} + r\sigma^2_{(yle)} + yr\sigma^2_{(lc)}$
LxE1	(l-1)(e1-1)	MS_{16}	$\sigma^2_{r(yle1)} + r\sigma^2_{(yle1)} + yr\sigma^2_{(le1)}$
LxE2	(l-1)(e2-1)	MS_{15}	$\sigma^2_{r(yle2)} + r\sigma^2_{(yle2)} + yr\sigma^2_{(le2)}$
LxE3	(l-1)(e3-1)	MS_{14}	$\sigma^2_{r(yle3)} + r\sigma^2_{(yle3)} + yr\sigma^2_{(le3)}$
LxE4	(l-1)(e4-1)	MS_{13}	$\sigma^2_{r(yle4)} + r\sigma^2_{(yle4)} + yr\sigma^2_{(le4)}$
Y x L x E	(y-1)(l-1)(e-1)	MS_{12}	$\sigma^2 + r\sigma^2_{(yle)}$
YxLxC	(y-1)(l-1)(c-1)	MS_{11}	$\sigma^2_{r(yle)} + r\sigma^2_{(yle)}$
YxLxE1	(y-1)(l-1)(e1-1)	MS_{10}	$\sigma^2_{r(yle1)} + r\sigma^2_{(yle1)}$
YxLxE2	(y-1)(l-1)(e2-1)	MS_9	$\sigma^2_{r(yle2)} + r\sigma^2_{(yle2)}$

Table 5. Continued

Source	df †	Mean Squares	Expected Mean Squares
YxLxE3	(y-1)(l-1)(e3-1)	MS_8	$\sigma^2_{r/yle3} + r\sigma^2_{yle3}$
YxLxE4	(y-1)(l-1)(e4-1)	MS_7	$\sigma^2_{r/yle4} + r\sigma^2_{yle4}$
Error	yl(r-1)(e-1)	MS_6	σ^2
R/YLC	yl(r-1)(c-1)	MS_5	$\sigma^2_{r/ylc}$
R/YLE1	yl(r-1)(e1-1)	MS_4	$\sigma^2_{r/yle1}$
R/YLE2	yl(r-1)(e2-1)	MS_3	$\sigma^2_{r/yle2}$
R/YLE3	yl(r-1)(e3-1)	MS_2	$\sigma^2_{r/yle3}$
R/YLE4	yl(r-1)(e4-1)	MS_1	$\sigma^2_{r/yle4}$

an approximate F test (McIntosh, 1983; Satterthwaite, 1946).

$$F = (MS_{30}+MS_{12})/(MS_{24}+MS_{18})$$

where:

MS_{30}= mean square associated with entries;

MS_{12}= mean square associated with the year x location x entry interaction;

MS_{24}= mean square associated with the year x entry interaction;

MS_{18}= mean square associated with the location x entry interaction;

Degrees of freedom (df) were calculated as follows:

$$N'df=(MS_{30}+MS_{12})^2/[(MS_{30})^2/(e-1)+(MS_{12})^2/(y-1)(l-1)(e-1)]$$

$$N''df= (MS_{24}+MS_{30})^2/[(MS_{24})^2/(y-1)(e-1)+(MS_{18})^2/(l-1)(e-1)]$$

where:

N' df= degrees of freedom for numerator;

N'' df= degrees of freedom for denominator.

The significance of the year x entry and the location x entry interactions was tested against the year x location x entry mean square (Table 5).

Phenotypic and rank correlation coefficients on an entry-mean basis for seed yield were calculated for hybrids over all selection criteria. Correlation coefficients on an entry-mean basis for the heterotic effects using MP and HP values were also calculated for hybrids over all selection

criteria. These correlations were obtained between all possible combinations of generations and plot types as follows:

1) F_1 planted in hills-F_2 planted in hills.

2) F_1 planted in hills-F_2 planted in row plots.

3) F_2 planted in hills-F_2 planted in row plots.

The PROC CORR and PROC CORR SPEARMAN in SAS (SAS User's Guide: Statistics, Version 5 Edition, 1985) were used to calculate the coefficients.

RFLP survey

Twenty four of the genotypes included in the study, three from each selection criterion and MG, were chosen to conduct a second determination of the RFLP pattern using 129 soybean genomic and cDNA probes. The genotypes were selected on the basis of the F_1 hybrid performance for seed yield evaluated during 1990. Two of the genotypes were chosen if their hybrid had seed yields significantly different from the MP and HP values. The third selected genotype was one that in combination with any of the other two, did not show significant heterosis expression. Exceptions were made for the ISO group of MGs II and III and the GO group of MG III in which cases low and high heterotic measures were used as the selecting criteria, because all hybrid combinations had significant heterotic effects.

The RFLP characterization was conducted at the DuPont DeNemours Co. laboratories. Laboratory procedures used at DuPont are reported in this study. Statistical analyses for the RFLP data were done at Iowa State University.

For the RFLP analysis, DNA was extracted from 3 g of lyopholized leaf tissue taken from 10 greenhouse-grown plants of a genotype following the method by Murray and Thompson (1980). For each genotype, a 5-ug sample of genomic DNA was digested individually with the restriction enzymes BamH1, EcoR1, EcoRV, Hind3 and Pst1, as well as with HpaII and Msp1. Blots containing parental DNA digested with Bcl1, Bgl2, Cfo1, Dra1, Msp1, Sca1, Ssp1, Xba1 were also used with cloned gene probes. Agarose gel electrophoresis and Southern blotting were carried out in standard conditions (Maniatis et al., 1982). DNA was transferred to GeneScreen (DuPont) or Hybond-N (Amersham) uncharged nylon membranes.

DNA probes were radiolabelled to approximately 10^9 cpm/ug DNA by random-primer synthesis of isolated inserts (Feinberg and Vogelstein, 1983). Fresh blots were prehybridized in 1M NaCl, 50 mM Tris-HCl pH 7.5, 1% SDS, 5% dextran sulphate, for several hours at 65° C. One hundred and twenty-five microliters of solution containing 75% formamide, 2.5 mg/ml of sheared, boiled, salmon testes carrier DNA and 1% SDS were added to the ^{32}P-labelled probe (50ul). The probe was denatured by incubating this mixture at 65° C for 15 min, and then added to the pre-hybridized blot. The hybridization was conducted at 65° C, during 20-24 hr, with gentle mixing in an air incubator. The blots were washed at 65° C, five times during 30 min, in the following solutions: 1. 2xSSPE, 0.1%SDS, 2. 2xSSPE, 0.1%SDS, 3. 2xSSPE, 1.0%SDS, 4.2xSSPE, 1.0%SDS, 5. 0.5xSSPE, 0.1%SDS (20xSSPE is 3.6 M NaCl, 200 mM NaH2PO4 pH 7.4, 20 mM EDTA (pH 7.4) (Maniatis et al., 1982)). Blots were placed in polypropylene project folders (C-line Products) and autoradiographed using Kodak X-Omat AR film, for 18-100 hrs. Blots were re-

used up to ten times, after stripping in 0.4N NaOH (30 min at 42° C) and washing in 0.2 M Tris-HCl pH 7.5, 0.1xSSPE, 0.1%SDS (30 min 42° C).

The soybean genomic probes used for the RFLP analysis were derived from genomic soybean DNA digested with the methylation-sensitive restriction enzyme PstI. Only low copy number genomic clones were used as probes. With the exception of the genes SAC (from R. Meagher, University of Georgia), PD1 (from P. Scolnik, DuPont Nemours Co.), and DS1 now called RPS24.1 (from N. Yadav, DuPont Nemours Co.), most probes were anonymous PstI genomic clones derived by DuPont Nemours Co.

Bands for each parent profile from the autoradiograms were coded 1 for the presence or 0 for the absence of the band. With the RFLP information provided genetic distance (GD_M) between all pairs of parents was estimated by applying the method developed by Nei and Li (1979), i.e.,

$$S_{XY} = 2N_{XY}/(N_X+N_Y)$$

where:

S_{XY}= measure of genetic similarity between a pair of parents;

N_{XY}= number of bands common to parents X and Y;

N_X and N_Y= number of bands for parents X and Y, respectively.

GD_M was then calculated as $1-S_{XY}$. Regression and correlation coefficients of GD_M on mean performance and heterotic effects of the F_1 hybrids grown in hill plots were calculated (SAS, 1985).

Relationships among parents based upon RFLP information were determined by a cluster analysis. The cluster diagram was constructed using the average linkage clustering algorithm (SAS, 1985) on the genetic distance matrix.

RESULTS

Maturity Group II

There was a significant year effect on HT and PROT content in the hill plot experiment (Table 6). Locations were also significantly different for HT. The year x location interaction was significant for YLD and SDWT, which was due to a difference in the magnitude of the response in the two years of evaluation, the Ames location had lower YLD and SDWT than Burkey. There were significant differences among entries and among selection criteria for all the traits. Except for MAT, LDG, PROT, and OIL measured in the HY group and OIL measured in the ISO group, variation among entries within selection criteria was significant for all traits in the four selection criteria. The two-way interactions of year x entries and location x entries were significant for some of the traits. The three-way interaction of year x location x entries was significant only for YLD and SDWT.

In the row plot experiment, years and locations had no significant effect on any of the traits (Table 6). The year x location interaction however, was significant for all traits except maturity. For YLD, LDG, HT, SDWT, and OIL, the interaction was significant due to different magnitudes in the response in the two years of evaluation. Similarly to the hill plot experiments, the Ames location had lower results than the Burkey location. For FLW and PROT, the interaction was significant due to a change in the direction of response in the two years of evaluation, the Ames location had lower values than Burkey in 1990, the opposite occurred during 1991. There

Table 6. Mean squares from the analysis of variance for traits measured in the hill and row plot experiments combined over years and locations for MG II

Source of variation	df§	Traits †							
		YLD	MAT	LDG	HT	FLW	SDWT	PROT	OIL
		g m^{-2}	days	score	cm	days	g 100^{-1}	--- g kg^{-1} ---	
					Hill Plot ‡				
Year (Y)	1	277567.7	48.1	3.72	27653.3*	2085.7	1485.80	875.30*	61.10
Location (L)	1	123226.9	98.3	12.80	4180.0*	5.5	230.60	2.17	0.04
Y*L	1	87335.9*	86.9	0.18	0.8	45.8	182.20*	3.96	0.87
Rep/Y/L	4	3509.3*	12.8*	2.56*	132.4*	11.1*	3.03*	1.06	0.67
Entries (E)	68	13613.8*	47.6*	2.23*	572.1*	64.4*	44.40*	17.05*	5.62*
Among Criteria	3	163428.8*	433.9*	24.60*	4665.2*	397.1*	291.50*	185.40*	83.60*
Within HY	15	6065.3*	16.0	0.41	204.9*	28.8*	5.32*	1.06	0.78
Within RFLP	17	7128.2*	19.7*	0.81*	221.4*	30.3*	13.74*	4.93*	1.56*
Within ISO	16	8767.5*	23.0*	0.76*	650.3*	45.3*	78.95*	14.00*	0.83
Within GO	17	4882.9*	58.5*	2.67*	450.9*	89.1*	33.50*	16.40*	4.70*
Y*E	68	2309.0*	6.4*	0.42	55.5	6.4*	1.96	1.15*	0.66*
L*E	68	1118.6	3.9	0.29	45.9	4.4	1.11	0.48	0.26
Y*L*E	68	1429.6*	3.3	0.35	42.7	4.2	1.49*	0.49	0.33
Error	272	907.5	3.2	0.32	47.8	3.4	0.81	0.51	0.55
					Row Plot ‡				
Year (Y)	1	7281.9	74.7	9.34	3391.7	634.7	232.80	114.92	16.50

* Significant at the 0.05 probability level.

† YLD= Seed yield; MAT= Days to physiological maturity; LDG= Lodging score; HT= Plant height; FLW= Days to flowering; SDWT= 100-seed weight; PROT= Protein content; OIL= Oil content.

‡ In the hill plot experiments, parents, F_1 hybrids, and F_2 bulks repeated twice in every replication were evaluated. In the row plot experiments, parents and F_2 bulks were evaluated.

§ df= Degrees of freedom.

Table 6. (Continued)

Source of variation	df§	Traits † YLD	MAT	LDG	HT	FLW	SDWT	PROT	OIL
		g m^{-2}	days	score	cm	days	g 100^{-1}	--- g kg^{-1} ---	
					Row Plot ‡				
Location (L)	1	94449.2	4.9	28.90	9211.2	71.1	199.80	15.10	5.20
Y*L	1	1758.7*	28.9	3.40*	1030.2*	88.0*	42.90*	13.40*	1.90*
Rep/Y/L	4	211.7	8.9	0.25	72.9*	1.5	0.45	0.54	0.20
Entries (E)	44	25738.6*	78.3*	2.12*	842.9*	43.3*	44.90*	16.70*	5.60*
Among Criteria	3	294001.2*	463.9*	13.40*	3495.4*	215.8*	155.60*	103.94*	46.00*
Within HY	9	3264.1	47.2*	0.28	172.0*	21.6*	6.86*	1.82*	0.28
Within RFLP	11	5449.5*	43.0	0.49	333.4*	9.0	9.04*	5.20*	1.74
Within ISO	10	6884.3*	40.6	0.70	929.1*	15.6*	109.10*	18.90*	3.08*
Within GO	11	8393.6*	68.3*	3.50*	1099.8*	73.6*	23.60*	14.50*	4.99*
Y*E	44	2529.5*	13.8*	0.37	68.8	7.1*	2.98*	1.24*	0.74*
L*E	44	1107.6	6.6	0.30	26.1	3.4	1.49	0.52	0.30
Y*L*E	44	1191.2*	6.4	0.24*	55.1*	2.4	1.19	0.39	0.30
Error	176	766.4	4.5	0.15	26.9	2.0	0.92	0.42	0.37

were significant differences for all traits among entries and among selection criteria. Except for YLD, LDG, and OIL measured in the HY group, MAT, LDG, FLW, and OIL in the RFLP group, and MAT and LDG in the ISO group, the variation among entries within selection criteria was significant for all other traits in the four selection criteria. The year x entry and the year x location x entry interactions were significant for some of the traits.

The midparent heterosis (MPH) mean values evaluated in the hill-plot experiment for seed yield were significant at individual years and combined over environments for all selection criteria indicating superiority of the F_1 hybrids over the MP (Table 7). In the combined data, the ISO selection criterion had the highest MPH at the F_1 generation, followed by the GO selection criterion. The MPH values for the HY and RFLP groups were similar and smaller than the other two. In the combined data, the six hybrids of the ISO and GO groups were significantly different to their respective MP values, two and three of the hybrids in the HY and RFLP selection criteria were also significant. Overall 17 of the 24 F_1 hybrids or 71% were significantly different to their respective MP values.

The high-parent heterosis (HPH) mean values for seed yield of the F_1 hybrids were significant in both years and combined only for the ISO and GO selection criteria (Table 7). For the HY selection criterion, significant differences to the HP value were observed only in 1990. No significant differences were observed for the RFLP group. Similar to the MPH values, the highest HPH mean values for yield at the F_1 generation evaluated in both years were observed for the ISO selection criterion. In the combined

Table 7. F_1 hybrid midparent and high-parent heterosis means for seed yield in grs m^{-2} and number of F_1 hybrids significantly different to the midparent or high-parent value for the four selection criteria of Maturity Group II

Criterion§	Parameter†	1990	1991	Combined
HY	$MPHF_1$ Mean	55*	25*	40*
	$HPHF_1$ Mean	44*	17	31
	No. F_1 > MP	2	2	2
	No. F_1 > HP	1	1	1
RFLP	$MPHF_1$ Mean	34*	44*	39*
	$HPHF_1$ Mean	-1	17	8
	No. F_1 > MP	0	3	3
	No. F_1 > HP	0	0	0
ISO	$MPHF_1$ Mean	66*	72*	69*
	$HPHF_1$ Mean	56*	49*	52*
	No. F_1 > MP	6	5	6
	No. F_1 > HP	4	2	5
GO	$MPHF_1$ Mean	37*	65*	51*
	$HPHF_1$ Mean	29*	49*	39*
	No. F_1 > MP	5	5	6
	No. F_1 > HP	2	4	4
Overall	Totals: ‡			
	No. F_1 > MP	13	15	17
	No. F_1 > HP	7	7	10

* F_1 group mean higher than the midparent or high-parent value at the 0.05 probability level.

† MPH= Midparent heterosis; HPH= High-parent heterosis; MP= Midparent; HP= High-parent; No.= Number of F_1 hybrids higher than MP or HP values.

‡ No.= Number of F_1 hybrids of the total twenty four higher than the MP or HP values.

§ HY= High yield; RFLP= Restriction fragment length polymorphism; ISO= Isozyme; GO= Geographic origin.

data, five, four, and one of the hybrids in the ISO, GO, and HY groups, respectively, were significantly different to their respective HP values. No F_1 hybrids better than the higher-yielding parent were observed in the RFLP group. Overall, 10 of the 24 F_1 hybrids or 42% were significantly superior in yield to the HP value.

For the F_2 bulks grown in hills, the ISO and GO selection criteria had the highest significant MPH mean values for seed yield combined over environments (Table 8). The MPH values of the HY and RFLP selection criteria were not significant. In the row-plot experiment, the GO group had the highest significant MPH value for seed yield over the two years. The MPH estimates obtained in row plots for the other groups were lower and not significant. None of the HPH mean values for seed yield were significant.

No trend was observed on the number of F_2 bulks grown in both hill and row plots significantly higher than the MP or HP value in any of the two years (Table 8). In the combined data, only the GO and ISO selection criteria had F_2 bulks grown in hills significantly higher than the MP value. In the row plot experiment, two F_2 bulks in the GO group and one in the HY and ISO groups yielded better than their respective MP value. None of the F_2 bulks in the RFLP group had better yields than the MP value. In the data combined over environments, only one F_2 bulk grown in hills from the ISO group yielded better than the HP value, none was observed in the row plot experiment. Overall, six bulks in the hill plot and four in the row plot experiments were significantly different to their respective MP value. Only one bulk in the hill plot experiment was superior to the HP value of the cross.

Table 8. F_2 bulk midparent and high-parent heterosis means for seed yield in grs m^{-2} and number of F_2 bulks significantly different to the midparent or high-parent value for the four selection criteria of Maturity Group II

Criterion§	Parameter†	1990		1991		Combined	
		Hill	Row	Hill	Row	Hill	Row
HY	$MPHF_2$ Mean	16	28	24*	13	21	21
	$HPHF_2$ Mean	6	15	16	-11	11	2
	No. F_2 > MP	0	2	0	0	0	1
	No. F_2 > HP	0	0	0	0	0	0
RFLP	$MPHF_2$ Mean	15	7	12	12	14	9
	$HPHF_2$ Mean	-20	-18	-16	-9	-18	-14
	No. F_2 > MP	0	0	1	1	0	0
	No. F_2 > HP	0	0	0	0	0	0
ISO	$MPHF_2$ Mean	21	15	29*	8	25*	12
	$HPHF_2$ Mean	10	-11	5	-16	8	-14
	No. F_2 > MP	0	1	1	1	1	1
	No. F_2 > HP	0	0	1	0	1	0
GO	$MPHF_2$ Mean	19	24	32*	38*	25*	31*
	$HPHF_2$ Mean	11	10	16	7	14	9
	No. F_2 > MP	2	1	4	2	5	2
	No. F_2 > HP	1	0	0	0	0	0
Overall	Totals: ‡						
	No. F_2 > MP	2	4	6	4	6	4
	No. F_2 > HP	1	0	1	0	1	0

* F_2 bulk group mean higher than midparent value at 0.05 probability level.

† MPH= Midparent heterosis; HPH= High-parent heterosis; MP= Midparent; HP= High-parent; No.= Number of F_2 bulks higher than MP or HP values.

‡ No.= Number of F_2 bulks of the total twenty four higher than the MP or HP values.

§ HY= High yield; RFLP= Restriction fragment length polymorphism; ISO= Isozyme; GO= Geographic origin.

Phenotypic and rank correlation coefficients for mean seed yield performance on an entry-mean basis across selection criteria and years for the three combinations of generations and plot types were high, significant, and positive (Table 9). These values indicate that in general, relative ranking of genotypes is similar for both generations (F_1 or F_2) and plot types (hill- or row-plots). The correlation coefficients of heterotic effects for seed yield were lower than for mean seed yield performance. The significant coefficients observed between F_1 hill-F_2 hill, and F_2 hill-F_2 row however, suggest that similar relative ranking of individuals may be expected for both generations evaluated in the same plot type, and for the F_2 generation grown in rows and hills. No correlation was observed of heterotic effects for seed yield between the F_1 hill and F_2 row data. This indicates that selection of superior hybrid individuals is not possible when generations and plot types are different.

The MPH mean values for MAT indicated that for some of the selection criteria, the F_1 hybrids and F_2 bulks had the tendency to mature later than the MP value (Table 10). For LDG, the F_1 hybrids and F_2 bulks had scores that were similar to the calculated MP value. Most of the F_1 hybrids and F_2 bulks were significantly taller than the MP value. For FLW, the MPH significant values for the F_1 hybrids in the HY, RFLP, and ISO selection criteria indicated that they flowered later than the MP. The F_2 bulks of the ISO group grown in hills and the F_2 bulks of the GO group grown in rows had significant and negative MPH values for FLW indicating that some bulks flowered earlier than the MP value.

Table 9. Phenotypic and rank correlation coefficients for seed yield mean performance, and midparent and high-parent heterotic effects for yield of F_2 hybrids and F_2 bulks of Maturity Group II grown in hills and hill- and row-plots, across selection criteria and environments

Correlated Combination	Mean Performance		MP †		HP †	
	Phenotypic	Rank	Phenotypic	Rank	Phenotypic	Rank
F_2 hill - F_2 hill	0.83*	0.75*	0.53*	0.56*	0.69*	0.68*
F_2 hill - F_2 row	0.71*	0.65*	0.04	0.12	0.18	0.29
F_2 hill - F_2 row	0.93*	0.94*	0.50*	0.53*	0.44*	0.50*

* Significant at the 0.05 probability level.
† MP= Midparent; HP= High-parent.

Table 10. F_1 hybrid and F_2 bulk midparent heterosis means for maturity, lodging, height, 100-seed weight, protein, and oil and number of F_1 hybrids and F_2 bulks significantly different to the midparent value for the four selection criteria of Maturity Group II, over environments

Criterion‡	Parameter§	G¶	Plot	Traits † MAT	LDG	HT	FLW	SDWT	PROT	OIL
				days	score	cm	days	$g100^{-1}$	--g kg^{-1}--	
HY	MPH Mean	F_1	Hill	0.9	0.3	5.7*	1.4*	0.2	1.0	1.0
		F_2	Hill	0.7	0.3	3.7*	0.1	-0.6	2.0	-3.0*
		F_2	Row	-0.1*	0.1	1.6*	-1.5	-0.7	-5.0	-2.0
RFLP		F_1	Hill	0.7	-0.1	3.8*	1.3*	0.3	-2.0	2.0*
		F_2	Hill	0.7*	0.1	3.8*	-0.5	-0.4	-2.0	1.0
		F_2	Row	1.6*	0	5.1*	-0.2	-0.8*	2.0	-2.0
ISO		F_1	Hill	1.7*	0.1	7.3*	1.4*	0.3	1.0	-2.0
		F_2	Hill	1.4*	0	4.7*	-1.2*	-0.2	2.0	-2.0
		F_2	Row	2.2*	0.2	8.4*	-0.8	-0.4*	2.0	-4.0*
GO		F_1	Hill	0.8	0	3.9*	0.5	0.2	-1.0	1.0
		F_2	Hill	1.7	0.1	3.2	-0.3	-0.2	2.0	0
		F_2	Row	2.4*	0.1	10.6*	-1.7*	-0.3	3.0	-1.0
Overall	No. > MP	F_1	Hill	5	4	6	6	2	-	1
		F_2	Hill	6	2	7	-	1	-	1
		F_2	Row	5	2	12	-	-	1	-

* F_1 hybrid or F_2 bulk group mean significantly different to the midparent value at the 0.05 probability level.

† MAT= Days to physiological maturity; LDG= Lodging score; HT= Plant height; FLW= Days to flowering; SDWT= 100-seed weight; PROT= Protein content; OIL= Oil content.

‡ HY= High yield; RFLP= Restriction fragment length polymorphism; ISO= Isozyme; GO= Geographic origin.

§ MPH= Midparent heterosis; MP= Midparent; No.= Number of F_1 hybrids or F_2 bulks of the total twenty four higher than the MP value.

¶ G= Generation.

Most MPH values for SDWT indicated no superiority of the F_1 hybrids and F_2 bulks over the MP values (Table 10). When individual hybrid populations were tested, a large frequency of F_2 bulks grown in hill and row plots was observed that were significantly lower in SDWT than the HP value (data not shown). The MPH values for PROT and OIL indicated that there were no F_1 hybrids and F_2 bulks with protein and oil content greater than the MP values. In individual hybrid combinations, most of the observed significant differences for PROT and OIL indicated that the F_1 hybrids and F_2 bulks had less protein and oil content (data not shown). The F_1 hybrids of the RFLP group were the only ones with a significant and positive OIL heterosis over the MP value.

Maturity Group III

There was a significant year effect on HT, FLW, and PROT content in the hill plot experiment (Table 11). The year x location interaction was significant for YLD, LDG, and SDWT. For YLD, the interaction was significant due to a different magnitude of response, YLD was higher in 1990 than in 1991. The Ames location was less yielding than Burkey. For LDG and SDWT, there was a difference in the direction of the response in the two years, the Ames location giving lower and higher results than the Burkey location in 1990 and in 1991, respectively. There were significant differences among entries and among selection criteria for all the traits. Except for YLD, MAT, LDG, HT, and FLW measured in the HY group, LDG and HT in the RFLP group, SDWT in the ISO group, and OIL in the GO group, variation among entries within selection criteria was significant for all other traits in the four selection criteria. The year x entry interaction

Table 11. Means squares from the analysis of variance for traits measured in the hill plot and row plot experiments combined over years and locations for MG III

Source of variation	df§	Traits †							
		YLD	MAT	LDG	HT	FLW	SDWT	PROT	OIL
		g m^{-2}	days	score	cm	days	g 100^{-1}	--- g kg^{-1} ---	
					Hill Plot ‡				
Year (Y)	1	137299.3	282.6	1.39	29392.7*	4836.9*	290.70	1428.04*	50.58
Location (L)	1	169915.6	3.0	0.21	3430.0	68.2	86.09	1.11	2.21
Y*L	1	31063.5*	6.7	6.50*	144.1	16.0	203.51*	4.34	6.24
Rep/Y/L	4	1713.2	12.4*	0.49	185.5*	27.7*	5.52*	2.47*	1.89*
Entries (E)	68	25468.7*	30.2*	3.65*	1229.1*	96.3*	23.21*	15.51*	10.98*
Among Criteria	3	367622.7*	89.0*	50.24*	10872.4*	1206.0*	107.11*	107.17*	125.95*
Within HY	15	3974.0	2.1	0.21	49.7	8.6	11.74*	1.79*	1.89*
Within RFLP	15	15797.8*	35.4*	0.82	133.6	57.5*	18.51*	14.98*	9.08*
Within ISO	18	9055.6*	27.6*	2.15*	275.5*	31.2*	3.83	12.09*	8.96*
Within GO	17	9966.3*	42.9*	2.54*	2544.5*	81.1*	43.17*	7.50*	2.52
Y*E	68	2570.8*	4.1*	0.53*	208.4*	11.9*	1.90*	1.15*	0.87*
L*E	68	1802.1	3.4*	0.25	86.7*	7.8	1.04*	0.63	0.78
Y*L*E	68	1610.7	1.9	0.23	54.3	6.2	0.65	0.48	0.52
Error	272	1270.5	1.9	0.32	60.3	6.0	0.79	0.62	0.63
					Row Plot ‡				
Year (Y)	1	33217.9	21.5	22.50	6864.4	3940.2	16.49	357.40	63.84

* Significant at the 0.05 probability level.

† YLD= Seed yield; MAT= Days to physiological maturity; LDG= Lodging score; HT= Plant height; FLW= Days to flowering; SDWT= 100-seed weight; PROT= Protein content; OIL= Oil content.

‡ In the hill plot experiments, parents, F_1 hybrids, and F_2 bulks repeated twice in every replication were evaluated. In the row plot experiments, parents and F_2 bulks were evaluated.

§ df= Degrees of freedom.

Table 11. (Continued)

Source of variation	df§	Traits † YLD	MAT	LDG	HT	FLW	SDWT	PROT	OIL
		g m^{-2}	days	score	cm	days	g 100^{-1}	--- g kg^{-1} ---	
					Row Plot ‡				
Location (L)	1	11533.4	94.0	1.88	1822.5	60.0	115.37	8.25	0.24
Y*L	1	38902.2	141.9*	4.67*	263.5	97.1*	85.40*	4.56	0.76
Rep/Y/L	4	6464.8*	14.7*	0.08	107.9*	6.7	0.53	0.75	0.63
Entries (E)	44	36041.6*	41.1*	3.87*	1753.6*	75.1*	26.00*	15.67*	14.23*
Among Criteria	3	374767.9*	15.9	24.80*	10458.7*	547.7*	66.74*	64.02*	89.66*
Within HY	9	3341.0	3.4	0.18	145.3*	6.9	13.62*	1.05	2.27*
Within RFLP	9	15665.7*	80.3*	1.28*	348.1*	36.9*	19.43*	21.64*	14.67*
Within ISO	12	6001.2*	38.9*	3.02*	234.4*	23.0	4.55*	14.92*	11.96*
Within GO	11	19859.1*	48.9*	4.22*	3430.7*	89.9*	53.80*	10.37*	5.55*
Y*E	44	1933.5*	8.2*	0.35*	163.4*	15.3*	0.92	1.26*	0.53
L*E	44	730.2	1.5	0.23	30.4	3.4	1.00	0.42	0.52
Y*L*E	44	858.4*	3.1*	0.17*	43.5	4.3	0.74	0.33	0.57
Error	176	578.9	1.6	0.11	30.4	3.0	0.57	0.48	0.72

was significant for all the traits, and the location x entry interaction was significant for MAT, HT, and SDWT. The three-way interaction of year x location x entry was not significant for any of the traits.

In the row plot experiment, years and locations had no significant effects on any of the traits (Table 11). The year x location interaction however, had significant effects on MAT, LDG, FLW, and SDWT. For MAT, LDG, and FLW the difference was in the direction of response in the two years of evaluation, the Ames location being later for MAT and earlier for FLW than Burkey in 1990, the opposite occurring in 1991. LDG was less at Ames than Burkey in 1990, Burkey however was worst than Ames in 1991. For SDWT, there was a difference in the magnitude of the response in the two years, Ames had SDWT that were smaller than Burkey in both years. There were significant differences for all traits among entries, and among selection criteria. Except for YLD, MAT, LDG, FLW, and PROT measured in the HY group, and FLW in the ISO group, variation among entries within selection criteria was significant for all traits in the four selection criteria. The year x entry interaction was significant for all traits except SDWT and OIL. The year x location x entry interaction was significant for YLD, MAT, and LDG.

The F_1 MPH mean for seed yield of each selection criterion were different in the two years of evaluation (Table 12). No significant MPH mean values were observed for the evaluation conducted during 1991. Significant differences between MPH and MP values however, were observed for the HY, RFLP, and GO selection criteria in 1990. Combined over environments, the ISO selection criterion had the highest MPH mean value.

Table 12. F_2 hybrid midparent and high-parent heterosis means for seed yield in grs m^{-2} and number of F_2 hybrids significantly different to the midparent or high-parent value for the four selection criteria of Maturity Group III

Criterion§	Parameter†	1990	1991	Combined
HY	$MPHF_2$ Mean	55*	14	34*
	$HPHF_2$ Mean	36	-2	16
	No. F_2 > MP	2	0	3
	No. F_2 > HP	2	0	0
RFLP	$MPHF_2$ Mean	45*	8	25
	$HPHF_2$ Mean	8	-26	-7
	No. F_2 > MP	2	2	2
	No. F_2 > HP	0	0	0
ISO	$MPHF_2$ Mean	54	50	50*
	$HPHF_2$ Mean	25	7	16
	No. F_2 > MP	3	3	5
	No. F_2 > HP	1	0	2
GO	$MPHF_2$ Mean	66*	35	49*
	$HPHF_2$ Mean	46*	-4	22
	No. F_2 > MP	5	3	5
	No. F_2 > HP	3	0	0
Overall	Totals: ‡			
	No. F_2 > MP	12	8	15
	No. F_2 > HP	6	0	2

* F_2 group mean higher than the midparent or high-parent value at the 0.05 probability level.

† MPH= Midparent heterosis; HPH= High-parent heterosis; MP= Midparent; HP= High-parent; No.= Number of F_2 hybrids higher than MP or HP values.

‡ No.= Number of F_2 hybrids of the total twenty four higher than the MP or HP values.

§ HY= High yield; RFLP= Restriction fragment length polymorphism; ISO= Isozyme; GO= Geographic origin.

followed by the GO and the HY selection criteria. The RFLP group had the lowest MPH mean which was not significant. Overall, 15 of the 24 F_1 hybrids or 62% were significantly higher in yield than the MP value. The largest frequency of individual F_1 hybrid combinations was observed in the ISO and GO selection criteria, 5 of the 6 F_1 hybrids in each group.

The F_1 HPH means for each selection criterion were also different in value for the two years of evaluation, and most of them were not significant (Table 12). Few F_1 hybrids were significantly higher in yield than the higher-yielding parent of each cross. Overall, only two of the 24 hybrids were significantly higher in yield than the HP value, and they were observed in the ISO selection criterion.

The MPH and HPH means for the F_2 bulks grown in hill and row plots were not significant, indicating no superiority of the F_2 bulks over the MP and HP values (Table 13). When individual F_2 bulks were considered, only a few on each selection criterion were significantly higher in yield than the MP value and most of them were observed in the row plots. The largest number was observed in the GO group, and of these only one F_2 bulk in 1991 was significantly higher in yield than the HP value.

The correlation coefficients for the three combinations of generations and plot types for mean seed yield performance across selection criteria were high, significant and positive, indicating that the relative ranking of individuals is similar for both generations and plot types (Table 14). The correlation coefficients of heterotic effects for seed yield were lower than for mean seed yield performance. The significant coefficient of MP heterotic effects for seed yield for the combination F_1

Table 13. F_2 bulk midparent and high-parent heterosis means for seed yield in grs m^{-2} and number of F_2 bulks significantly different to the midparent or high-parent value for the four selection criteria of Maturity Group III

		1990		1991		Combined	
Criterion§	Parameter†	Hill	Row	Hill	Row	Hill	Row
HY	$MPHF_2$ Mean	22	14	12	-6	18	4
	$HPHF_2$ Mean	3	-5	-5	-21	-1	-13
	No. F_2 > MP	1	1	0	0	1	0
	No. F_2 > HP	0	0	0	0	0	0
RFLP	$MPHF_2$ Mean	26	17	-5	0	11	8
	$HPHF_2$ Mean	-13	-28	-40	-30	-26	-29
	No. F_2 > MP	1	0	0	0	0	1
	No. F_2 > HP	0	0	0	0	0	0
ISO	$MPHF_2$ Mean	14	7	22	11	18	9
	$HPHF_2$ Mean	-13	-21	-24	-9	-17	-14
	No. F_2 > MP	0	1	0	0	1	0
	No. F_2 > HP	0	0	0	0	0	0
GO	$MPHF_2$ Mean	25	22	11	16	18	19
	$HPHF_2$ Mean	5	-10	-29	-38	-12	-24
	No. F_2 > MP	2	3	0	3	0	3
	No. F_2 > HP	0	0	0	1	0	1
Overall	Totals: ‡						
	No. F_2 > MP	4	5	0	3	2	4
	No. F_2 > HP	0	0	0	1	0	1

† MPH= Midparent heterosis; HPH= High-parent heterosis; MP= Midparent; HP= High-parent; No.= Number of F_2 bulks higher than MP or HP values.

‡ No.= Number of F_2 bulks of the total twenty four higher than the MP or HP values.

§ HY= High yield; RFLP= Restriction fragment length polymorphism; ISO= Isozyme; GO= Geographic origin.

Table 14. Phenotypic and rank correlation coefficients for seed yield mean performance, and midparent and high-parent heterotic effects for yield of F_1 hybrids and F_2 bulks of Maturity Group III grown in hills and hill- and row-plots, across selection criteria and environments

Correlated Combination	Mean Performance		MP †		HP †	
	Phenotypic	Rank	Phenotypic	Rank	Phenotypic	Rank
F_1 hill - F_2 hill	0.93*	0.93*	0.60*	0.55*	0.74*	0.72*
F_1 hill - F_2 row	0.93*	0.95*	0.39	0.43*	0.57*	0.46*
F_2 hill - F_2 row	0.95*	0.93*	0.27	0.22	0.42*	0.44*

* Significant at the 0.05 probability level.
† MP= Midparent; HP= High-parent.

hill-F_2 hill suggests that similar ranking of individuals may be expected for the two generations in the same plot type. These may not be observed when different generations are grown in different plot types, and when the F_2 generation is evaluated in different field plot arrangements. The coefficients of HP heterotic effects for seed yield for the three combinations however, suggest that similar ranking of genotypes may be expected for both generations and plot types.

The MPH mean for MAT for the RFLP and GO selection criteria indicated that the F_1 hybrids and F_2 bulks matured later than the MP value (Table 15). No significant heterotic effects were observed for the HY group, for the ISO group the F_2 bulks grown in rows were significantly later than the MP value. For LDG, most of the MPH means in the F_1 hybrids and F_2 bulks were not different to the MP values. In the ISO group however, the F_1 hybrids and F_2 bulks in hills lodged significantly less than the MP value although the size of this difference may be too small to be of practical value. Except for the F_2 bulks grown in hills of the ISO selection criterion, the MPH mean for HT of the ISO and GO groups indicated that hybrids were significantly taller than the MP value. No significant differences in plant HT were observed in the HY and RFLP selection criteria. For FLW, significant MPH means in the F_1 were observed in the RFLP, ISO, and GO selection criteria. These F_1 hybrids were later in flowering than the MP value.

Mean SDWT for each criterion was similar to the calculated MP values (Table 15). When individual hybrid populations were tested, a large frequency of F_1 hybrids and F_2 bulks significantly lower in SDWT than the

Table 15. F_1 hybrid and F_2 bulk midparent heterosis means for maturity, lodging, height, 100-seed weight, protein, and oil and number of F_1 hybrids and F_2 bulks significantly different to the midparent value for the four selection criteria of Maturity Group III, over environments

Criterion‡	Parameter§	G¶	Plot	Traits † MAT	LDG	HT	FLW	SDWT	PROT	OIL
				days	score	cm	days	$g100^{-1}$	--g kg^{-1}--	
HY	MPH Mean	F_1	Hill	0.3	0.1	2.4	0.4	0.5	0	1.0
		F_2	Hill	0.3	0	3.1	-0.7	0.4	1.0	-1.0
		F_2	Row	0.3	0	5.6	-0.1	0.1	0	1.0
RFLP		F_1	Hill	1.4*	-0.2	2.0	4.1*	0.3	1.0	1.0
		F_2	Hill	2.2*	-0.2	2.4	1.0	-0.2	3.0	-2.0
		F_2	Row	2.8*	0.2	1.9	-1.3	-0.3	3.0	-5.0*
ISO		F_1	Hill	0.6	-0.1*	6.7*	1.2*	0.8	9.0*	-8.0*
		F_2	Hill	0.6	-0.2*	2.7	-0.5	0.5	7.0*	-9.0*
		F_2	Row	1.4*	0	2.8*	-1.2	0.2	10.0*	-7.0*
GO		F_1	Hill	1.6*	0.4	16.8*	1.4*	0	1.0	-4.0
		F_2	Hill	1.8*	0.2	11.6*	-0.8	0.1	2.0	-4.0
		F_2	Row	1.3*	0.3	15.9*	-1.1	-0.5	1.0	-7.0*
Overall	No. > MP	F_1	Hill	5	3	5	6	6	5	1
		F_2	Hill	6	1	3	-	2	4	-
		F_2	Row	10	2	11	-	-	6	-

* F_1 hybrid or F_2 bulk group mean significantly different to the midparent value at the 0.05 probability level.

† MAT= Days to physiological maturity; LDG= Lodging score; HT= Plant height; FLW= Days to flowering; SDWT= 100-seed weight; PROT= Protein content; OIL= Oil content.

‡ HY= High yield; RFLP= Restriction fragment length polymorphism; ISO= Isozyme; GO= Geographic origin.

§ MPH= Midparent heterosis; MP= Midparent; No.= Number of F_1 hybrids or F_2 bulks of the total twenty four higher than the MP value.

¶ G= Generation.

HP value was however, observed (data not shown). Except for the F_1 hybrids and F_2 bulks in the ISO group, the MPH means for PROT in the HY, RFLP, and GO groups did not differ from the MP value. The observed significant MPH means for OIL indicated that some of the F_1 hybrids and F_2 bulks had less OIL content than the MP value. Similar to SDWT, there was a large frequency of F_1 hybrids and F_2 bulks that were significantly lower in PROT and OIL contents than the HP value (data not shown).

RFLP Survey

During the evaluations conducted in 1990 it was observed that for seed yield some genotypes were included in hybrid combinations with heterotic effects and also in some combinations with no heterotic effects (Table 17). This pattern was not observed in all selection criteria such as the ISO group of MG II and III and the GO group of MG III. It was also observed that hybrids within the RFLP selection criteria did not show the highest heterotic effects for yield (Tables 7, 8, 12, and 13). In order to assess the genetic relationship between these genotypes and heterosis expression, 24 genotypes were sampled to determine the RFLP pattern.

The RFLP-based genetic distance (GD_M) estimates among the 24 genotypes ranged from 14 (Beeson 80 x Asgrow25AF) to 46% (Zane x PI82.235) (Table 16). For all possible hybrids including combinations not obtained for evaluation in this study, the lowest GD_M estimates were obtained between the genotypes released from the US soybean pool, i.e., Elgin 87 x Beeson 80 (19%), Williams 82 x BSR 301 (15%), Resnik x Conrad (15%), and Williams 82 x Sherman (18%). The highest GD_M values were generally obtained between a US-released genotype and a plant introduction, i.e., Zane x

Table 16. Genetic distance (%) matrix determined by RFLP analysis

Genotypes	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
1. KENWOOD	0																							
2. ASGROW25AF	28	0																						
3. BEESON 80	28	14	0																					
4. BSR 301	22	34	32	0																				
5. CLOUD	37	38	44	36	0																			
6. CONRAD	25	23	29	26	37	0																		
7. DUNFIELD	32	32	33	35	36	34	0																	
8. ELGIN 87	18	22	19	29	38	20	31	0																
9. FUNMAN	39	36	33	36	30	34	29	27	0															
10. HAROSOY	28	27	27	32	45	23	32	19	31	0														
11. ILLINI	30	26	28	30	36	29	29	30	36	30	0													
12. PI54.592	37	24	26	35	33	30	25	27	26	26	28	0												
13. PI61.940	35	29	23	31	35	34	27	28	24	33	29	24	0											
14. PI80.671	31	33	26	27	38	31	34	27	28	26	29	30	25	0										
15. PI82.235	33	35	33	43	37	37	37	36	41	34	38	32	36	34	0									
16. RESNIK	29	27	34	28	34	15	34	24	28	30	33	32	34	34	40	0								
17. SENECA	37	29	26	40	36	35	26	31	30	32	29	27	28	28	34	40	0							
18. SHERMAN	26	25	24	21	36	15	35	20	34	27	27	34	32	27	37	23	27	0						
19. TASTEE	31	34	29	40	39	34	36	31	34	33	35	32	31	29	19	38	27	36	0					
20. ZANE	32	36	31	28	38	27	31	24	31	35	31	35	31	29	46	31	29	22	44	0				
21. WILLIAMS 82	27	34	31	15	35	27	30	28	30	31	31	36	32	26	42	27	31	18	39	20	0			
22. PI437.477B	24	28	25	27	34	30	27	26	32	33	24	26	26	29	35	31	34	33	33	29	28	0		
23. MUKDEN	34	22	22	41	35	36	33	28	30	31	30	28	24	31	28	35	21	30	28	37	39	27	0	
24. RICHLAND	33	26	25	32	40	33	32	30	37	31	30	27	29	35	35	36	33	29	29	44	32	32	28	0

Table 17. F_1 hybrids per selection criterion of Maturity Groups II and III that had significant and not significant heterotic effects for seed yield during 1990 and the RFLP-based genetic distance estimates between the genotypes of the F_1 hybrids

Criterion†	Parentage of Hybrid	GD_M ‡	MPH §		HPH §	
			1990	C	1990	C
		%	--------- g m^{-2} --------			
		MG II ¶				
HY	Kenwood x Conrad	26	102*	93*	97*	85*
	Kenwood x Elgin 87	18	26	17	10	7
RFLP	Harosoy x Seneca	32	59*	45*	57*	45
	Asgrow25AF x Seneca	29	7	30	-17	5
ISO =	Beeson 80 x Mukden	22	72*	65*	72*	44*
	Beeson 80 x Funman	33	46*	52*	30	45*
GO	PI80.671 x Tastee	30	50*	66*	48*	61*
	PI80.671 x Richland	34	14	38*	4	28*
		MG III ¶				
HY	Sherman x Resnik	23	72*	43*	56*	27
	Resnik x Zane	31	30	44*	30	39
RFLP	Dunfield x Illini	29	57*	51*	46	32
	PI437.477B x Dunfield	27	24	20	2	18
ISO =	BSR 301 x Cloud	36	83*	54*	66*	31
	Williams 82 x Cloud	35	57*	36*	16	-18
GO =	PI54.940 x PI54.592	24	60*	60*	51*	51
	PI54.592 x PI82.235‡	32	38*	13	18	-2

* F_1 hybrid significantly superior in yield to the midparent value and the high-parent of the cross at the 0.05 probability level.

† HY= High yield; RFLP= Restriction fragment length polymorphism; ISO= Isozyme; GO= Geographic origin.

‡ GD_M= Genetic distance estimates.

§ MPH= Midparent heterosis; HPH= High-parent heterosis; C= Combined data.

¶ MG II= Maturity Group II; MG III= Maturity Group III.

= Low and high heterotic measures were used as the selecting criteria.

Richland (44%), Zane x Tastee (44%), Beeson 80 x Cloud (44%), BSR 301 x PI82.235 (43%), and Zane x PI82.235 (46%).

For the hybrids evaluated in this study, the lowest GD_M was calculated for Kenwood and Elgin 87 of MG II in the HY group, 18% (Tables 16 and 17). This can be related to the pedigree of both cultivars of which the cultivar Elgin is a common immediate ancestor (Cianzio et al., 1990; Fehr et al., 1988). The highest GD_M estimate calculated was obtained between BSR 301 and Cloud of MG III in the ISO group, 36%. The ISO criterion averaged a GD_M over MGs of 32% which was the highest, the GO averaged 30% and 29% the RFLP group. The HY group had the lowest GD_M average, 24% (Table 17).

The relationship between GD_M estimates and seed yield heterosis and yield per se was determined (Table 18). Correlations were low, negative, and nonsignificant. These results indicate that for the group of genotypes used in the study, yield heterosis and seed yield per se cannot be predicted by using an estimate of genetic distance based on RFLP markers. In general, the GD_M estimate between two genotypes was not related with with heterotic effects for seed yield (Table 17). For instance in the combined data of MG III, for the GO selection criterion a GD_M estimate of 24% corresponded to a significant MPH, and an estimate of 32% did not. In the RFLP criterion of MG II, a GD_M estimate of 32% had significant MPH for 1990 and combined, and significant HPH for 1990. In the same criterion a GD_M of 29% did not have any heterotic effects. Also the sizes of the GD_M estimates were not related to the relative magnitude of the heterotic effects, i.e. a 97 g m^{-2} high-parent heterotic effect for the hybrid

Table 18. Correlation and determination coefficients between RFLP-based genetic distance and midparent and high-parent heterotic effects for seed yield and seed yield per se of F_1 hybrids over selection criteria, Maturity Groups, and environments

	Heterotic Effects For Seed Yield		Seed Yield Per Se
	F_1MP ‡	F_1HP ‡	F_1 Hybrids
Genetic distance			
Correlation † Coefficient	0.08	-0.18	-0.29
Coefficient of † Determination	0.8%	3%	8%

† Coefficients were obtained over all hybrid combinations in which the genotypes sampled for the RFLP pattern were included.
‡ MP= Midparent; HP= High-parent.

Kenwood x Conrad of the HY criterion of MG II was obtained with a GD_M of 26%. In the ISO criterion of MG III, a GD_M estimate of 35% for the cross Williams 82 x Cloud, had a high-parent heterotic effect of 16 g m^{-2}.

The genetic relationship among the genotypes included in the survey and those in the specific hybrid combinations was determined by a cluster analysis based on the genetic distance matrix (Figure 1). Four main groups were distinguished in the dendrogram. The first included genotypes released from the US soybean pool (Kenwood, Elgin 87, Harosoy, Conrad, Sherman, Resnik, BSR 301, Williams 82, and Zane). The second group included introduced genotypes (PI54.592, Richland, Seneca, Mukden, Dunfield, Illini, PI437.477B, PI61.940, Funman, and PI80.671) and two genotypes released from the US soybean pool (Asgrow25AF and Beeson 80). The third group included two plant introductions (PI82.235 and Tastee), and Cloud, a plant introduction, formed the fourth group, proving to be different from all other genotypes.

The genotypes included in the HY selection criterion (Kenwood, Elgin 87, Conrad, Sherman, Resnik, and Zane) of both MGs tended to be close to each other in the dendrogram (Figure 1). This grouping explained the low GD_M mean obtained for the HY selection criterion (Table 17). The cluster analysis showed a clear grouping of the RFLP genotypes of MG III (Dunfield, Illini, and PI437.477B). For the RFLP group of MG II however, the genotypes Asgrow25AF, Seneca, Harosoy, and Richland were not grouped as close to each other as for MG III. In general, the genotypes of the ISO and GO groups were apart in the dendrogram. The four highest GD_M estimates were obtained for pairs of genotypes in the ISO (Cloud x BSR 301, Williams 82 x Cloud,

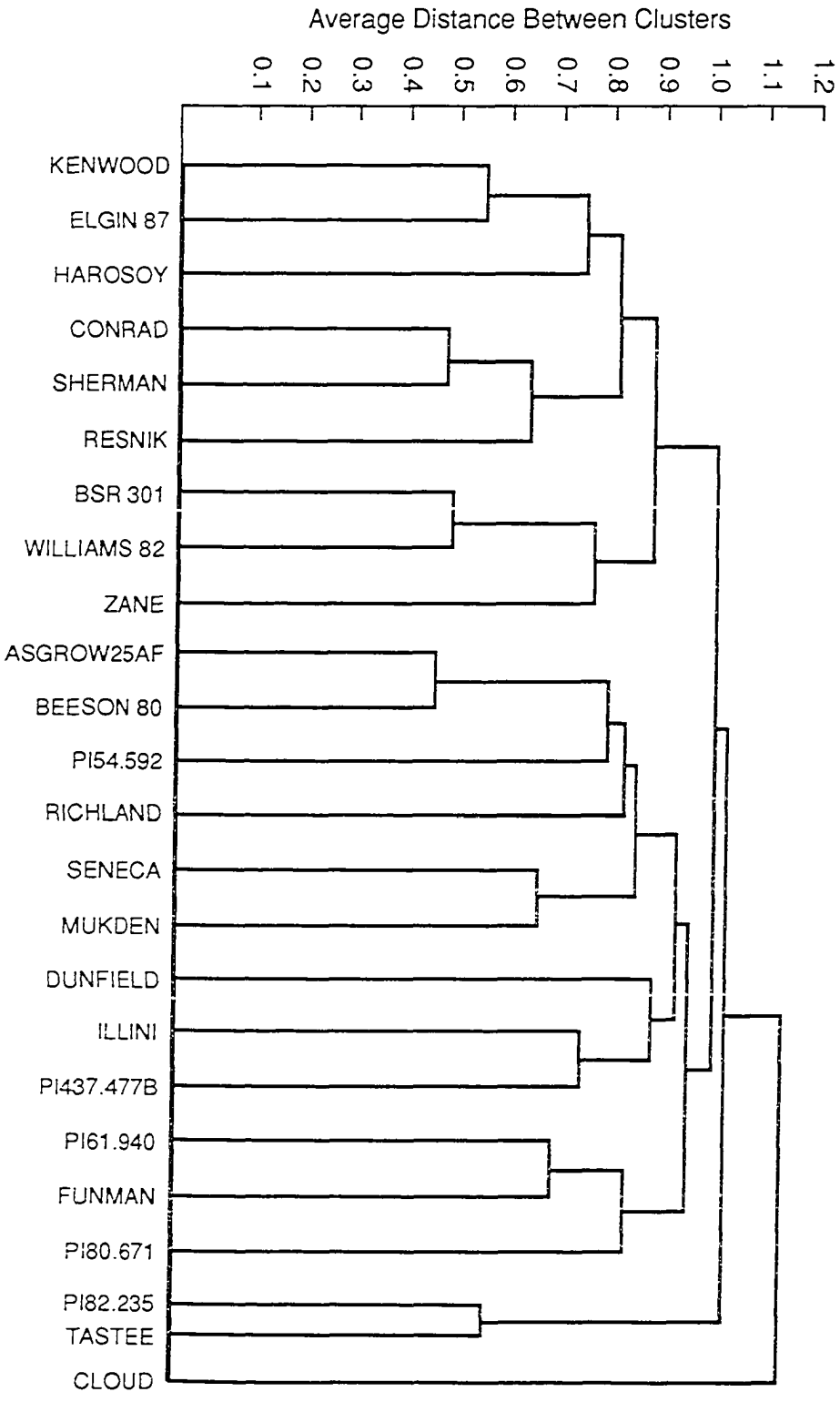

Figure 1. Association of soybean genotypes as revealed by cluster analysis of genetic distance estimates from RFLP data

Beeson 80 x Funman) and GO (PI80.671 x Richland) groups (Table 17). The dendrogram revealed no close relationship between any of the genotypes included in these pairs (Figure 1). This result suggests that genetic diversity as indicated by six-isozyme loci and geographic origin were in this study better predictors of heterotic performance than the selection criteria used for the HY and RFLP groups.

DISCUSSION

In the work reported herein, the F_1 hybrids in the ISO group had higher MPH and HPH values over the other three criteria. Hybrid combinations derived from parents differing at six isozyme loci also showed the largest frequency of F_1 hybrids significantly superior in yield to the calculated MP and the HP value. These results indicate that for the group of crosses evaluated in this study, the differences in genetic diversity as expressed by 6 isozyme loci were effective in predicting F_1 hybrid performance. Price et al. (1986) and Lamkey et al. (1987) in maize found that isozyme allelic differences between inbred lines were not predictive of hybrid performance.

The F_1 heterotic effects for yield in the GO selection criterion always followed those found in the ISO selection criterion, indicating that diversity of geographic origin was important in the heterosis expression observed in this study. Similar results have been obtained by Moll et al. (1965) in maize, Niehaus and Pickett (1966) and Malm (1968) in sorghum, Parker et al. (1970) in peanuts, Vandenberg and Matzinger (1970) in tobacco, and Matzinger and Frakes (1973) in tall fescue. These studies suggested that geographically diverse parents should produce more vigorous hybrids than parents of similar geographic origins. This was not observed in the study by Paschal and Wilcox (1975) in soybean in which they evaluated hybrid combinations of 10 parental origins including parents that were adapted cultivars, and plant introductions from the same and different geographic origin. The authors reported that genotypes from the same

geographic area produced the hybrids with the highest heterotic effects for yield.

The RFLP selection criterion had the lowest average heterosis performance, in both MPH and HPH values, except for the MG II MPH value in 1991. The parents for this group were selected from a survey of 58 wild and cultivated accessions conducted by Keim et al. (1989). At the time of the survey, 17 RFLPs were used to establish the genotype of each accession, of which 11 were finally used because some of the other markers had little variation generating only small amounts of information (Keim et al., 1989). From the data obtained in the present work, it appears that the use of 11 RFLP loci was not effective in establishing genetic distances among the genotypes to predict hybrid performance. The close clustering of the RFLP genotypes of MG III for instance, suggested that more than 11 RFLP markers may be needed to obtain these estimates. Keim et al. (1992) in a later study concluded that for estimating RFLP-based genetic distances in soybean, a minimum of 65 marker loci should be used. The number of RFLP markers available in soybean has greatly increased (Keim et al., 1990). If genotypes were to be selected with the RFLP information presently available, it could be speculated that different findings might have been observed for the RFLP group.

In my study, the coefficients of correlation and determination obtained between RFLP-based genetic distance calculated as proposed by Nei and Li (1979) in a sample of genotypes using 129 RFLP markers, and heterotic effects for seed yield and seed yield per se at the F_1 generation indicated a poor association for these traits. Similar results have been

reported in maize in which the correlation of hybrid performance with molecular marker diversity between parents has been too low to be of any predictive value (Dudley et al., 1991; Godshalk et al., 1990; Lee et al., 1989; Melchinger et al., 1990). The results suggest that measures of genetic distances calculated from RFLP data may not provide the type of genetic information required to predict hybrid performance.

In general, the low frequency of F_1 hybrids significantly different from the MP and HP values indicated that selecting genotypes for crossing on the basis of the yielding performance per se may not be effective to predict significant heterotic effects. Previous studies on heterotic effects in soybean have been conducted by crossing high-yielding parents released from the US gene pool (Nelson and Bernard, 1984; Weber et al., 1970). Nelson and Bernard (1984) found significant but low heterosis effects for all traits considered, with the level of expression generally lower than previously reported. Weber et al. (1970), in a previous study evaluating hybrids obtained by crossing high-yielding lines, found significant superiority of F_1 hybrids over the midparent and high-parent values.

The results for seed yield obtained in the F_2 bulks did not follow any trend in the size of the heterosis effects measured and in the number of individuals significantly different to the MP and HP values. In general, except for the GO F_2 bulks of MG II and III grown in hill and row plots, there were few significant differences between hybrid performance of the F_2 bulks compared to the MP and HP values and these differences varied in number according to selection criteria and plot types. The F_1 generation

was evaluated in hill plots only, and the F_2 in both hill and row plots. The correlation coefficients based on mean yield performance indicated that either generation and plot type can be used for yield evaluation. The low frequency of F_2 generation bulks significantly different from the MP and HP values indicated, however, that the use of only the F_2 generation to evaluate heterotic effects may not be effective for hybrid production.

The results of the study also indicated that date of flowering, date of maturity, and plant height of F_1 hybrids and F_2 bulks was generally intermediate between the MP and the later flowering and maturing, and the taller parent. For date of flowering and of maturity similar results have been reported previously (Brim and Cockerham, 1961; Chaudhary and Singh, 1974; Leffel and Weiss, 1958; Weber et al., 1970; Weiss et al., 1947), and also for plant height (Brim and Cockerham, 1961; Kalton, 1948; Paschal and Wilcox, 1975; Veatch, 1930; Weber et al., 1970). Small, and mostly nonsignificant heterotic effects were observed for plant lodging in the study. Similar results were reported by Nelson and Bernard (1984) and also by Paschal and Wilcox (1975).

Small heterotic effects were observed for seed weight, and protein and oil content. A large frequency of the F_1 hybrids and F_2 bulks were significantly lower in seed weight, protein, and oil content than the high-parent value. Previous studies have also reported similar findings for seed weight (Chaudhary and Singh, 1974; Leffel and Weiss, 1958; Paschal and Wilcox, 1975; Veatch, 1930; Weber et al., 1970) and for protein and oil content (Nelson and Bernard, 1984; Weber et al., 1970).

SUMMARY AND CONCLUSIONS

The use of different criteria for selection and crossing of genotypes to maximize heterosis expression of seed yield, agronomic and seed traits was evaluated in this work. Two criteria at the molecular level, RFLP and isozyme constitution were compared to selection of parents on the basis of yielding ability and of different geographic origin. Seed-yielding ability was used because it is the major trait considered by soybean breeders for the development of improved cultivars. Diversity in geographic origin was used because it has been defined as a key to genetic diversity and to hybrid vigor itself (Moll et al., 1965). The two criteria at the molecular level were evaluated because these markers express loci differences among genotypes and therefore may be used as a measure of genetic diversity (Lander and Botstein, 1989; Tanksley, 1983).

The results of the study indicated that of the two criteria at the molecular level, selecting parents for different isozyme constitution was more advantageous for the expression of heterosis in seed yield than the use of RFLP genetic distances. It was also more advantageous than selecting parents on the basis of yielding ability and than on the basis of diverse geographic origin. For both MGs and for the genotypes included in the study, the hybrids in the isozyme criterion had higher midparent and high-parent heterosis expression than the other groups. The number of F_1 hybrid combinations superior to the calculated midparent value and to the high-parent genotype of each cross were also larger than for the other selection criteria. These results suggest that for soybean, differences in genetic

constitution expressed by or linked to isozyme loci may be effective predictors of heterotic expression in F_1 hybrids.

Geographic origin of soybean genotypes may also be considered in planning crosses. In general in the study, the F_1 hybrids obtained from crossing parents of diverse geographical areas had heterotic effects that were second in size to the isozyme group, and also in the number of F_1 hybrids superior to the midparent value and the high-parent genotype of the cross.

The RFLP selection criterion had in general the smallest average heterosis expression measured as midparent and high-parent heterosis, except for the midparent heterosis value of MG II during 1991. The genotypes for this criterion were selected and crossed according to genetic distances calculated by using 11 RFLP markers (Keim et al., 1989). The results observed in my study suggest that in soybean, the measure of genetic distances calculated from RFLP data may not be effective in establishing the genetic information required for the prediction of hybrid performance. This finding was further supported by the results from a second RFLP characterization conducted in a sample of the genotypes used in this research, purposedly selected to maximize differences in hybrid performance. In the sample, no relationship could be detected between the RFLP-based genetic distance of the genotypes crossed and performance of the F_1 hybrids.

No trend in heterosis estimates was observed in the F_2 bulks, indicating that evaluations on the basis of only F_2 generation would not be of value to predict heterotic hybrid performance in the F_1 generation. In

general, few significant differences between hybrid performance of the F_2 bulks compared to the MP and HP values were observed and these differences varied in number according to selection criteria and plot types. The evaluations conducted in the F_1 and F_2 generations in hill and row plots of both MGs however, suggested that midparent heterotic effects determined at the F_2 generation in hills could be of value to predict the F_1 hybrid heterotic performance if they also were planted in hill plots. The top high-yielding heterotic F_1 hybrids could be predicted from this type of yield test. This information could then be used to determine the hybrid combinations in which efforts will be directed to obtain the number of F_1 seed required to conduct more extensive testing at the F_1 generation. No association was observed between heterotic expression in the F_2 generation in rows and in the F_1 generation planted in hills.

The results of this study also indicated that date of flowering, date of maturity, and plant height of F_1 hybrids and F_2 bulks was generally intermediate between the MP and the later flowering and maturing, and the taller parent. Small, and mostly nonsignificant heterotic effects were also observed for plant lodging, and for seed weight, and protein and oil content.

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APPENDIX A. MEANS OF GENOTYPES FOR SEED YIELD, DAYS TO PHYSIOLOGICAL MATURITY, LODGING, HEIGHT, DAYS TO FLOWERING, SEED WEIGHT, AND PROTEIN AND OIL CONTENT

Table A1. Mean seed yield (g m^{-2}) of parents, F_1 hybrids, and F_2 bulks of the four selection criteria of Maturity Group II grown in hill and row plot experiments conducted in 1990 and 1991

Entry	Generation	1990 Hill	1990 Row	1991 Hill	1991 Row	Combined Hill	Combined Row
		High Yield					
Hack	Parent	187	336	238	338	212	337
Elgin 87		224	384	261	375	242	379
Conrad		209	357	267	431	238	394
Kenwood		193	374	251	387	222	380
Elgin 87 x Hack	F_1	246		280		263	
	F_2	187	388	266	394	226	391
Conrad x Elgin 87	F_1	283*		274		278	
	F_2	236	400	268	366+	252	383
Kenwood x Conrad	F_1	303*+		343*+		323*+	
	F_2	231	400	304	413	267	406
Kenwood x Elgin 87	F_1	234		265		250	
	F_2	225	379	278	418	252	399
Hack x Kenwood	F_1	247		193		220	
	F_2	215	402*	266	353	240	377
Conrad x Hack	F_1	237		319*		278*	
	F_2	231	384*	285	430	258	407*
		Restriction Fragment Length Polymorphism					
Asgrow25AF	Parent	215	343	272	361	243	352
Richland		128	285	166	293	147	289
Corsoy		117	329	264	373	191	351
A80-244036		215	368	296	358	255	363
Seneca		167	268	217	318	192	293
Harosoy		163	296	219	366	191	331
Asgrow25AF x Corsoy	F_1	183		288		236	
	F_2	188	354	251	370	219	362
Corsoy x A80-244036	F_1	224		283		254	
	F_2	180	346	286	374	233	360
Harosoy x Seneca	F_1	224		249		237*	
	F_2	177	292	221	327	199	309
Seneca x Asgrow25AF	F_1	198		298		248	
	F_2	194	310	244	344	219	327
Richland x Asgrow25AF	F_1	224		309		267*	
	F_2	188	329	265*	350	227	340
A80-244036 x Richland	F_1	184		297		241*	
	F_2	196	322	264	375*	230	349

* Significantly different from midparent value at the 0.05 probability level.
+ Significantly different from high-parent value at the 0.05 probability level.

Table A1. Continued

Entry	Generation	1990 Hill	1990 Row	1991 Hill	1991 Row	Combined Hill	Combined Row
		Isozyme					
Magna	Parent	151	309	173	216	162	263
Mukden		163	259	155	285	159	272
Funman		195	298	230	304	213	301
Bansei		181	253	154	242	168	248
Beeson 80		162	327	238	333	200	330
Mukden x Magna	F_1	214*+		286*+		250*+	
	F_2	175	296	231*+	315*	203*+	306*
Funman x Mukden	F_1	235*+		237		236*	
	F_2	192	296	233	264	207	280
Bansei x Magna	F_1	236*+		245*+		241*+	
	F_2	174	276	207	264	190	270
Beeson 80 x Mukden	F_1	234*+		255*		244*+	
	F_2	198	331*	213	310	205	320
Beeson 80 x Funman	F_1	225*		291*		258*+	
	F_2	202	338	249	333	225	335
Beeson 80 x Bansei	F_1	267*+		268*		268*+	
	F_2	198	295	196	251+	197	273+
		Geographic Origin					
Tastee	Parent	131	187	159	190	145	189
PI30.594		116	219	153	242	134	230
PI80.671		127	242	142	173	134	208
Richland		146	265	164	295	155	280
PI69.501		129	244	121	250	125	247
PI85.580		151	253	209	296	180	274
PI30.594 x PI69.501	F_1	159*		224*+		192*+	
	F_2	129	247	167*	283	148	265
PI30.594 x Tastee	F_1	166*+		171		169*	
	F_2	152*	232	171	242	161	237
PI69.501 x Richland	F_1	176*		228*+		202*+	
	F_2	156	277	183	279	169*	278
PI80.671 x PI84.580	F_1	176*		232*		204*	
	F_2	151	264	216*	311*	184*	288*
PI80.671 x Tastee	F_1	180*+		232*+		206*+	
	F_2	160*+	262*	173	199	166*	231
PI80.671 x Richland	F_1	150		217*+		183*+	
	F_2	153	269	198*	298*	175*	283*

Table A2. Mean number of days to physiological maturity (days after 31 August) of parents, F_1 hybrids, and F_2 bulks of the four selection criteria of Maturity Group II grown in hill and row plot experiments conducted in 1990 and 1991

Entry	Generation	1990		1991		Combined	
		Hill	Row	Hill	Row	Hill	Row
High Yield							
Hack	Parent	21	25	21	26	21	26
Elgin 87		21	21	20	20	20	21
Conrad		22	23	25	27	23	25
Kenwood		21	24	21	19	21	21
Elgin 87 x Hack	F_1	21		21		21	
	F_2	22	25	21	24	22	25
Conrad x Elgin 87	F_1	22		22		22	
	F_2	23*+	25*	23	24	23	24
Kenwood x Conrad	F_1	22		24		23	
	F_2	25*+	26*	22+	28*	23	27*
Kenwood x Elgin 87	F_1	21		21		21	
	F_2	22*	20	22+	22	20	22
Hack x Kenwood	F_1	21		24*+		22	
	F_2	21	24	19	20+	20	22+
Conrad x Hack	F_1	23*+		26*		24*	
	F_2	24*+	26*	24	29	24*	28
Restriction Fragment Length Polymorphism							
Asgrow25AF	Parent	21	25	24	26	22	26
Richland		20	21	22	23	20	22
Corsoy		18	20	19	22	19	21
A80-244036		22	23	22	26	22	24
Seneca		20	22	20	20	20	21
Harosoy		18	18	19	20	19	18
Asgrow25AF x Corsoy	F_1	20		22		21	
	F_2	20	24	22	23	21	24
Corsoy x A80-244036	F_1	21		20		21	
	F_2	22*	25*	20	24	21	25
Harosoy x Seneca	F_1	19		18		19	
	F_2	21	22*	20	21	20	22
Seneca x Asgrow25AF	F_1	24*+		24		24*	
	F_2	23*	25	25*	26	24*	25
Richland x Asgrow25AF	F_1	21		22		22	
	F_2	22	24	22	27	22	26
A80-244036 x Richland	F_1	21		22		22	
	F_2	19	24	20	24	20+	24

* Significantly different from midparent value at the 0.05 probability level.
\+ Significantly different from high-parent value at the 0.05 probability level.

Table A2. Continued

Entry	Generation	1990 Hill	1990 Row	1991 Hill	1991 Row	Combined Hill	Combined Row
		Isozyme					
Magna	Parent	18	17	22	24	20	20
Mukden		22	26	22	22	22	24
Funman		21	22	22	26	21	24
Bansei		22	21	21	22	22	22
Beeson 80		22	25	22	26	22	25
Mukden x Magna	F_1	20		22		21	
	F_2	20	20+	23	26	22	22
Funman x Mukden	F_1	25*+		26*+		25*+	
	F_2	23*	26	24	26	24*	26
Bansei x Magna	F_1	20		24*		22	
	F_2	22*	22*	22	27*	22	24*
Beeson 80 x Mukden	F_1	22		21		22	
	F_2	22	25	23	25	23	25
Beeson 80 x Funman	F_1	22		22		22	
	F_2	22	25	24	27	23	26
Beeson 80 x Bansei	F_1	26*+		28*+		27*+	
	F_2	24*+	28*	24*	29*	24*+	28*+
		Geographic Origin					
Tastee	Parent	22	21	19	19	20	20
PI30.594		12	15	15	16	14	15
PI80.671		14	10	14	16	14	13
Richland		20	21	23	23	22	22
PI69.501		16	17	18	19	17	18
PI85.580		24	24	22	22	23	23
PI30.594 x PI69.501	F_1	16		18		17	
	F_2	16	16	19	20	17	18
PI30.594 x Tastee	F_1	18+		19		19	
	F_2	23*	22*	22*	22*	22*	22*
PI69.501 x Richland	F_1	18		19+		18+	
	F_2	17	20	20	23	19	22
PI80.671 x PI84.580	F_1	19+		18+		18+	
	F_2	21+	19*+	19	19	20	19+
PI80.671 x Tastee	F_1	21*		22*		21*	
	F_2	22*	23*	21*	20	21*	22*
PI80.671 x Richland	F_1	15+		17+		16+	
	F_2	16+	18*+	17+	20	17+	19

Table A3. Mean lodging score (from 1= all plants erect to 5= all plants prostrate) of parents, F_1 hybrids, and F_2 bulks of the four selection criteria of Maturity Group II grown in hill and row plot experiments conducted in 1990 and 1991

Entry	Generation	1990		1991		Combined	
		Hill	Row	Hill	Row	Hill	Row
High Yield							
Hack	Parent	1.9	1.5	1.6	1.1	1.8	1.3
Elgin 87		2.2	1.2	2.2	1.4	2.2	1.3
Conrad		1.8	1.2	2.4	1.5	2.1	1.3
Kenwood		2.0	1.4	2.3	2.0	2.2	1.7
Elgin 87 x Hack	F_1	2.4		2.2		2.3	
	F_2	2.1	1.5	2.2	1.5	2.1	1.5
Conrad x Elgin 87	F_1	3.0*		2.2		2.6	
	F_2	2.6*+	1.6	2.4	1.8	2.5	1.7*+
Kenwood x Conrad	F_1	2.8*		2.2		2.5	
	F_2	2.2*+	1.8	2.6	2.0	2.4	1.9*
Kenwood x Elgin 87	F_1	2.1		2.5		2.3	
	F_2	2.2	1.4	2.7	1.8	2.4	1.6
Hack x Kenwood	F_1	2.5		1.4*+		1.9	
	F_2	2.2	1.6	2.2	1.4+	2.2	1.5
Conrad x Hack	F_1	2.5		2.4		2.4*	
	F_2	2.4	1.2	2.2	1.8*+	2.3	1.5
Restriction Fragment Length Polymorphism							
Asgrow25AF	Parent	2.2	1.9	2.5	1.9	2.4	1.9
Richland		2.1	2.2	2.4	2.2	2.2	2.2
Corsoy		2.0	2.1	3.1	2.4	2.6	2.2
A80-244036		3.1	2.4	3.1	2.0	3.1	2.2
Seneca		3.1	1.8	2.6	2.9	2.9	2.3
Harosoy		2.8	2.2	2.7	2.9	2.8	2.6
Asgrow25AF x Corsoy	F_1	1.6		2.2+		1.9	
	F_2	2.6	1.9	2.5	1.9	2.5	1.9
Corsoy x A80-244036	F_1	3.0		2.5		2.8	
	F_2	2.8	2.2	3.4	2.8*	3.1	2.5
Harosoy x Seneca	F_1	2.6		3.1		2.9	
	F_2	2.4	2.2	3.1	2.5	2.8	2.4
Seneca x Asgrow25AF	F_1	1.9+		2.8		2.3	
	F_2	2.4	2.2	2.8	2.6	2.6	2.4
Richland x Asgrow25AF	F_1	2.5		2.5		2.5	
	F_2	1.8	1.6	2.7	2.0	2.2	1.8
A80-244036 x Richland	F_1	2.9		2.8		2.8	
	F_2	3.2	2.5	2.7	2.0	2.9	2.2

* Significantly different from midparent value at the 0.05 probability level.
+ Significantly different from high-parent value at the 0.05 probability level.

Table A3. Continued

Entry	Generation	1990 Hill	1990 Row	1991 Hill	1991 Row	Combined Hill	Combined Row
		Isozyme					
Magna	Parent	2.0	1.1	3.0	2.5	2.5	1.8
Mukden		2.8	2.0	3.1	2.2	2.9	2.1
Funman		3.1	1.5	3.2	2.9	3.2	2.2
Bansei		2.1	1.6	1.8	1.5	1.9	1.6
Beeson 80		2.2	1.2	2.6	1.8	2.4	1.5
Mukden x Magna	F_1	2.1		2.9		2.5	
	F_2	2.1	1.6	2.9	1.8*+	2.5	1.7
Funman x Mukden	F_1	2.8		3.0		2.9	
	F_2	2.8	2.0	3.3	2.9	3.0	2.4
Bansei x Magna	F_1	3.0*		2.8		2.9*	
	F_2	2.4	1.4	2.9	2.8*	2.7	2.1
Beeson 80 x Mukden	F_1	2.4		2.6		2.5	
	F_2	2.1	1.6	2.5	1.9	2.3+	1.8
Beeson 80 x Funman	F_1	2.9		3.2		3.1	
	F_2	2.6*+	2.1	2.7	2.1+	2.7	2.1
Beeson 80 x Bansei	F_1	2.6		2.8		2.7*	
	F_2	2.4	1.6	2.8	2.4*	2.6	2.0
		Geographic Origin					
Tastee	Parent	2.1	1.1	2.2	1.2	2.2	1.2
PI30.594		4.5	3.8	4.6	4.0	4.6	3.9
PI80.671		3.2	2.0	3.1	2.1	3.2	2.1
Richland		2.0	2.0	3.1	2.4	2.6	2.2
PI69.501		3.9	2.4	3.6	2.8	3.8	2.6
PI85.580		2.8	2.5	3.5	2.9	3.1	2.7
PI30.594 x PI69.501	F_1	4.2		3.5+		3.9+	
	F_2	3.9	2.8+	4.1	3.1	3.9+	2.9+
PI30.594 x Tastee	F_1	3.6+		3.6+		3.6+	
	F_2	3.8+	2.6+	3.9	2.9+	3.9*+	2.8+
PI69.501 x Richland	F_1	2.6+		2.8+		2.7+	
	F_2	2.6+	2.4	3.4	2.8	3.0+	2.6
PI80.671 x PI84.580	F_1	3.2		2.9		3.1	
	F_2	3.0	2.4	3.2	2.2	3.1	2.3
PI80.671 x Tastee	F_1	3.4*		3.1		3.2*	
	F_2	2.9	1.4	3.2	2.1	3.0	1.8
PI80.671 x Richland	F_1	2.8		3.0		2.9	
	F_2	3.6*	2.2	3.1	2.4	3.4*	2.3

Table A4. Mean plant height (cm) of parents, F_1 hybrids, and F_2 bulks of the four selection criteria of Maturity Group II grown in hill and row plot experiments conducted in 1990 and 1991

Entry	Generation	1990		1991		Combined	
		Hill	Row	Hill	Row	Hill	Row
		High Yield					
Hack	Parent	81	87	92	95	86	91
Elgin 87		70	81	82	83	76	82
Conrad		78	88	86	96	82	92
Kenwood		73	90	84	96	78	93
Elgin 87 x Hack	F_1	79		93		86	
	F_2	77	91*	88	96	83	94*
Conrad x Elgin 87	F_1	78		89		84	
	F_2	75	92*	81	94	78	93*
Kenwood x Conrad	F_1	82		92		87*	
	F_2	80	97*	100*+	104	90*+	100*+
Kenwood x Elgin 87	F_1	76		83		80	
	F_2	74	84	84	94	79	88
Hack x Kenwood	F_1	82		92		87	
	F_2	81	92	94	94	87	93
Conrad x Hack	F_1	87		102*+		94*+	
	F_2	80	92	97*	96	89	94
		Restriction Fragment Length Polymorphism					
Asgrow25AF	Parent	84	94	98	106	91	100
Richland		74	89	90	94	82	92
Corsoy		81	88	102	102	92	94
A80-244036		76	81	86	84	81	82
Seneca		84	93	106	104	95	99
Harosoy		81	97	101	112	91	105
Asgrow25AF x Corsoy	F_1	80		102		91	
	F_2	82	99*+	100	104	91	101
Corsoy x A80-244036	F_1	86		96		91	
	F_2	81	92*	96	102	88	97*
Harosoy x Seneca	F_1	95*		104		100	
	F_2	87	96	106	108	97	102
Seneca x Asgrow25AF	F_1	84		114*		99	
	F_2	83	102*+	105	108	94	105
Richland x Asgrow25AF	F_1	84		96		90	
	F_2	83	96	109*	108	96*	102*
A80-244036 x Richland	F_1	76		90		83	
	F_2	82	88	96	96	89*	92*

* Significantly different from midparent value at the 0.05 probability level.
+ Significantly different from high-parent value at the 0.05 probability level.

Table A4. Continued

Population	Generation	1990 Hill	1990 Row	1991 Hill	1991 Row	Combined Hill	Combined Row
		Isozyme					
Magna	Parent	84	92	98	100	91	96
Mukden		94	96	97	109	95	102
Funman		78	86	100	94	89	90
Bansei		56	72	58	60	57	66
Beeson 80		78	96	94	104	86	100
Mukden x Magna	F_1	86+		101		93	
	F_2	88	100	100	104	94	102
Funman x Mukden	F_1	91		104		97	
	F_2	79*+	101*	103	106	90	104*
Bansei x Magna	F_1	82*		91*		86*	
	F_2	76*+	90*	92*	104*	84*+	97*
Beeson 80 x Mukden	F_1	87+		102		95	
	F_2	85+	101	102	104	94	103
Beeson 80 x Funman	F_1	81		98		90	
	F_2	83	98	98	101	90	99
Beeson 80 x Bansei	F_1	84*		98*		91*	
	F_2	79*	100*	91*	101*	85*	100*
		Geographic Origin					
Tastee	Parent	50	58	60	46	55	52
PI30.594		62	74	77	86	70	80
PI80.671		74	75	80	74	76	75
Richland		75	91	91	95	75	83
PI69.501		81	88	96	91	88	90
PI85.580		75	83	94	89	84	86
PI30.594 x PI69.501	F_1	72+		89		80+	
	F_2	70+	83	89	98*	80+	91
PI30.594 x Tastee	F_1	71*+		86*+		79*+	
	F_2	67*	83*+	80*	94*	74*	88*
PI69.501 x Richland	F_1	78		88		83	
	F_2	83	91	89	101	86	96
PI80.671 x PI84.580	F_1	71		87		79	
	F_2	72	77	84+	84	78+	80
PI80.671 x Tastee	F_1	66+		80*		73*	
	F_2	70*	91*+	77	86*+	74*	88*+
PI80.671 x Richland	F_1	75		90		83	
	F_2	76	89	88	90	82	90

Table A5. Mean number of days to flowering (days after June 30) of parents, F_1 hybrids, and F_2 bulks of the four selection criteria of Maturity Group II grown in hill and row plot experiments conducted in 1990 and 1991

Entry	Generation	1990		1991		Combined	
		Hill	Row	Hill	Row	Hill	Row
		High Yield					
Hack	Parent	11	11	9	11	10	11
Elgin 87		17	18	12	14	14	16
Conrad		18	17	14	14	16	16
Kenwood		17	16	13	14	15	15
Elgin 87 x Hack	F_1	15		11		13	
	F_2	15	14+	11	13	13	14+
Conrad x Elgin 87	F_1	20*		15		17*	
	F_2	17	16	13	15	15	16
Kenwood x Conrad	F_1	19		14		16	
	F_2	18	16	14	13	16	15
Kenwood x Elgin 87	F_1	18		14		16	
	F_2	18	17	12	14	14	15
Hack x Kenwood	F_1	13+		12		12+	
	F_2	15	13+	10+	12+	12+	12+
Conrad x Hack	F_1	18*		14		16*	
	F_2	15+	14+	11+	11*+	13+	13+
		Restriction Fragment Length Polymorphism					
Asgrow25AF	Parent	14	14	12	14	13	14
Richland		13	16	13	14	13	15
Corsoy		17	17	10	14	14	15
A80-244036		16	14	10	14	13	14
Seneca		21	20	14	14	18	17
Harosoy		14	14	10	14	12	14
Asgrow25AF x Corsoy	F_1	16		12		14	
	F_2	16	16	12	14	14	15
Corsoy x A80-244036	F_1	17		10		14	
	F_2	15	15+	10	13	13	14
Harosoy x Seneca	F_1	19		14		17	
	F_2	17+	19*	12	13	14+	16
Seneca x Asgrow25AF	F_1	24*		14		19*	
	F_2	17	17+	13	13	15+	15+
Richland x Asgrow25AF	F_1	16		12		14	
	F_2	14+	15	13	14	13	15
A80-244036 x Richland	F_1	16		12		14	
	F_2	13+	13+	10+	14	11	14

* Significantly different from midparent value at the 0.05 probability level.
+ Significantly different from high-parent value at the 0.05 probability level.

Table A5. Continued

Entry	Generation	1990 Hill	1990 Row	1991 Hill	1991 Row	Combined Hill	Combined Row
		Isozyme					
Magna	Parent	16	17	16	15	16	16
Mukden		21	20	15	16	18	18
Funman		19	20	16	17	17	18
Bansei		22	22	18	18	20	20
Beeson 80		18	18	16	15	17	17
Mukden x Magna	F_1	18		14		16	
	F_2	18	16*+	15	14	16	15*+
Funman x Mukden	F_1	27*+		18*+		23*+	
	F_2	19	19	15	15	17	17
Bansei x Magna	F_1	20		16		18	
	F_2	17+	20+	14*+	17	15*+	18
Beeson 80 x Mukden	F_1	18		14		16	
	F_2	19	18	15	15	17	16
Beeson 80 x Funman	F_1	18		14		16	
	F_2	17	18	14	15	15+	16
Beeson 80 x Bansei	F_1	27*+		20*+		24*+	
	F_2	21	22	15	15	18	18
		Geographic Origin					
Tastee	Parent	25	25	18	18	22	22
PI30.594		21	24	19	20	20	22
PI80.671		13	14	10	15	12	14
Richland		14	16	12	14	13	15
PI69.501		18	19	17	17	17	18
PI85.580		18	19	16	15	17	17
PI30.594 x PI69.501	F_1	20		17*		19	
	F_2	21	20+	16	16*+	19	18+
PI30.594 x Tastee	F_1	24		19		21	
	F_2	21	22	18	16*+	19+	19*+
PI69.501 x Richland	F_1	18		13*		15	
	F_2	16	16	13+	14+	14+	15+
PI80.671 x PI84.580	F_1	16		12*		14+	
	F_2	15	15+	12+	13	14+	14+
PI80.671 x Tastee	**F_1**	**21**		**18***		**19*+**	
	F_2	**19**	**19+**	**18***	**16+**	**18+**	**17+**
PI80.671 x Richland	**F_1**	**13**		**12**		**12**	
	F_2	13+	13	10	13	12	13

Table A6. Mean seed weight (g 100^{-1} seeds) of parents, F_1 hybrids, and F_2 bulks of the four selection criteria of Maturity Group II grown in hill and row plot experiments conducted in 1990 and 1991

Entry	Generation	1990 Hill	1990 Row	1991 Hill	1991 Row	Combined Hill	Combined Row
		High Yield					
Hack	Parent	17	17	20	20	18	18
Elgin 87		17	18	19	19	18	18
Conrad		15	16	18	17	17	16
Kenwood		15	16	18	16	17	16
Elgin 87 x Hack	F_1	18		20		19	
	F_2	17	18*	20	19	18	19
Conrad x Elgin 87	F_1	16		18		17	
	F_2	16	17+	17*+	16*+	17*+	16*+
Kenwood x Conrad	F_1	16		18		17	
	F_2	14	16	17*+	17	16*	16
Kenwood x Elgin 87	F_1	17		18		18	
	F_2	16	17	19	18	17	18
Hack x Kenwood	F_1	16		19		18	
	F_2	16	18*	19	18	17+	18
Conrad x Hack	F_1	16		19		18	
	F_2	16+	16	18+	18+	17*+	17
		Restriction Fragment Length Polymorphism					
Asgrow25AF	Parent	16	17	19	18	17	17
Richland		15	17	19	20	17	18
Corsoy		14	15	17	18	16	17
A80-244036		18	19	22	19	20	19
Seneca		14	15	17	18	16	16
Harosoy		16	16	18	18	17	18
Asgrow25AF x Corsoy	F_1	16		19		17	
	F_2	15+	16	18	18	16+	17
Corsoy x A80-244036	F_1	16+		18+		17*	
	F_2	16+	16+	18+	17	17*+	17*+
Harosoy x Seneca	F_1	15		18		17	
	F_2	15	16	18	18	17	17
Seneca x Asgrow25AF	F_1	15		18		16	
	F_2	15+	14*+	17+	16	16	15
Richland x Asgrow25AF	F_1	16		19		17	
	F_2	15+	15*+	18	17+	16+	16*+
A80-244036 x Richland	F_1	18*		22*		20*	
	F_2	17*	17+	21	19	19*+	18

* Significantly different from midparent value at the 0.05 probability level.
+ Significantly different from high-parent value at the 0.05 probability level.

Table A6. Continued

Entry	Generation	1990 Hill	1990 Row	1991 Hill	1991 Row	Combined Hill	Combined Row
		Isozyme					
Magna	Parent	25	28	29	26	27	27
Mukden		14	14	18	18	16	16
Funman		16	16	21	18	18	17
Bansei		22	23	24	23	22	23
Beeson 80		17	19	22	20	19	19
Mukden x Magna	F_1	20+		25+		22+	
	F_2	20+	21+	23+	22+	22+	22+
Funman x Mukden	F_1	15		19		17	
	F_2	15	15	18+	16	17+	16
Bansei x Magna	F_1	24		25+		25+	
	F_2	24	24*+	27+	26	25+	25+
Beeson 80 x Mukden	F_1	17		21		19*	
	F_2	16	17*+	20	19	18	18
Beeson 80 x Funman	F_1	17		20		18	
	F_2	17	17+	20	19	18	18+
Beeson 80 x Bansei	F_1	19+		22		21+	
	F_2	18+	19*+	21*+	20+	19*	19*+
		Geographic Origin					
Tastee	Parent	22	21	25	23	23	22
PI30.594		12	14	16	16	14	15
PI80.671		18	20	23	20	21	20
Richland		16	17	19	20	18	18
PI69.501		16	17	20	20	18	19
PI85.580		17	17	20	20	19	18
PI30.594 x PI69.501	F_1	16*		20*		18*	
	F_2	14+	15+	20	19	17+	17
PI30.594 x Tastee	F_1	16+		18*+		17*	
	F_2	17+	17+	20+	18+	19+	18+
PI69.501 x Richland	F_1	17		22*		20*	
	F_2	17	18	20	19	18	18
PI80.671 x PI84.580	F_1	17+		22		20	
	F_2	18	18	22	20	20	19
PI80.671 x Tastee	F_1	20+		24		22	
	F_2	19+	20	22*+	19*+	21*+	19*+
PI80.671 x Richland	F_1	16+		22+		19+	
	F_2	17+	18	21+	21	19+	20

Table A7. Mean protein content (g kg^{-1}) of parents, F_1 hybrids, and F_2 bulks of the four selection criteria of Maturity Group II grown in hill and row plot experiments conducted in 1990 and 1991

Entry	Generation	1990 Hill	1990 Row	1991 Hill	1991 Row	Combined Hill	Combined Row
		High Yield					
Hack	Parent	408	412	384	397	396	404
Elgin 87		406	406	392	390	399	398
Conrad		408	398	383	379	395	389
Kenwood		402	412	386	397	394	404
Elgin 87 x Hack	F_1	414*+		389		402	
	F_2	412	407	389	400	401	404
Conrad x Elgin 87	F_1	408		382		395	
	F_2	411	397	384	396*	397	396
Kenwood x Conrad	F_1	407		385		396	
	F_2	413*	406	376	389	394	398+
Kenwood x Elgin 87	F_1	414*+		389		401	
	F_2	415*+	400*+	389	398	402	399+
Hack x Kenwood	F_1	408		385		397	
	F_2	411*	406	387	394	399	399+
Conrad x Hack	F_1	406		372		389*	
	F_2	411	404	377*	387	394	396+
		Restriction Fragment Length Polymorphism					
Asgrow25AF	Parent	418	414	382	386	400	399
Richland		421	413	408	409	414	411
Corsoy		426	418	388	405	407	412
A80-244036		405	399	368	382	387	390
Seneca		425	413	404	404	415	409
Harosoy		427	427	403	414	415	420
Asgrow25AF x Corsoy	F_1	405*+		391		398+	
	F_2	417	410	385	399	401	404
Corsoy x A80-244036	F_1	406*+		382		394+	
	F_2	410+	409+	385*+	393+	397+	401+
Harosoy x Seneca	F_1	424		403		414	
	F_2	424	420	402	412	413	416
Seneca x Asgrow25AF	F_1	419		386*+		402+	
	F_2	420	417	388+	401	404	409
Richland x Asgrow25AF	F_1	414		396+		405+	
	F_2	422	416	388*+	399+	405+	407
A80-244036 x Richland	F_1	416+		392+		404+	
	F_2	413	412	386+	393+	399+	402+

* Significantly different from midparent value at the 0.05 probability level.
+ Significantly different from high-parent value at the 0.05 probability level.

Table A7. Continued

Entry	Generation	1990 Hill	1990 Row	1991 Hill	1991 Row	Combined Hill	Combined Row
		Isozyme					
Magna	Parent	409	402	398	394	404	398
Mukden		446	446	419	427	433	436
Funman		453	438	424	438	438	438
Bansei		410	402	398	404	404	403
Beeson 80		424	416	399	408	411	412
Mukden x Magna	F_1	432+		413		423+	
	F_2	430+	421+	404+	414+	417+	417+
Funman x Mukden	F_1	464*		419		442	
	F_2	452	448	422	428+	437	438
Bansei x Magna	F_1	411		387*		399	
	F_2	415	402	395	396	405	399
Beeson 80 x Mukden	F_1	439		406+		423+	
	F_2	437	435	411	419	424	427+
Beeson 80 x Funman	F_1	436+		405+		420+	
	F_2	443	439*	412+	419+	427+	429
Beeson 80 x Bansei	F_1	426		393		409	
	F_2	424	422*	398	408	411	415
		Geographic Origin					
Tastee	Parent	413	413	404	415	409	414
PI30.594		484	466	441	433	462	449
PI80.671		419	414	404	411	412	413
Richland		422	413	402	411	412	412
PI69.501		419	422	402	409	410	416
PI85.580		439	431	405	413	422	422
PI30.594 x PI69.501	F_1	448+		418+		433+	
	F_2	454+	456*	429+	439*	442+	448*
PI30.594 x Tastee	F_1	446+		419+		433+	
	F_2	442+	433+	416+	427	429+	430+
PI69.501 x Richland	F_1	428		400		414	
	F_2	427	417	408	413	418	415
PI80.671 x PI84.580	F_1	425+		407		416	
	F_2	436	424	408	413	422	418
PI80.671 x Tastee	F_1	416		395		406	
	F_2	418	410	398	414	408	412
PI80.671 x Richland	F_1	420		411		416	
	F_2	423	417	404	413	414	415

Table A8. Mean oil content (g kg^{-1}) of parents, F_1 hybrids, and F_2 bulks of the four selection criteria of Maturity Group II grown in hill and row plot experiments conducted in 1990 and 1991

Entry	Generation	1990		1991		Combined	
		Hill	Row	Hill	Row	Hill	Row
		High Yield					
Hack	Parent	219	209	219	214	219	212
Elgin 87		213	209	218	215	216	212
Conrad		210	213	222	214	216	214
Kenwood		220	208	216	210	218	209
Elgin 87 x Hack	F_1	209+		217		213+	
	F_2	213	209	218*+	211	215	209
Conrad x Elgin 87	F_1	212		222		217	
	F_2	210	209	215	206*+	212	208*+
Kenwood x Conrad	F_1	216		225*		220	
	F_2	204*+	207	218	216	211*+	211
Kenwood x Elgin 87	F_1	214		219		216	
	F_2	206*+	208	216	211	211*+	209
Hack x Kenwood	F_1	218		219		219	
	F_2	217	212	219	214	218	213
Conrad x Hack	F_1	218		225*		222	
	F_2	210+	207	221	218	216	212
		Restriction Fragment Length Polymorphism					
Asgrow25AF	Parent	206	204	215	214	210	209
Richland		204	208	206	205	205	206
Corsoy		197	199	216	208	207	204
A80-244036		216	212	223	216	219	214
Seneca		200	199	206	199	203	199
Harosoy		199	189	211	202	205	196
Asgrow25AF x Corsoy	F_1	212*		216		214*	
	F_2	207	201	213	212	210	207
Corsoy x A80-244036	F_1	214*		217		216	
	F_2	209	201+	219	209+	214+	205+
Harosoy x Seneca	F_1	200		208		204	
	F_2	201	202	211	201	206	201
Seneca x Asgrow25AF	F_1	210*+		211		211	
	F_2	204	200	209	201*+	207+	201
Richland x Asgrow25AF	F_1	209		214		212	
	F_2	204	201	211	209	208	205
A80-244036 x Richland	F_1	207+		212+		209+	
	F_2	208	204	213+	205+	210+	205+

* Significantly different from midparent value at the 0.05 probability level.
+ Significantly different from high-parent value at the 0.05 probability level.

Table A8. Continued

Entry	Generation	1990 Hill	1990 Row	1991 Hill	1991 Row	Combined Hill	Combined Row
		Isozyme					
Magna	Parent	204	201	198	202	201	201
Mukden		193	182	205	199	199	191
Funman		191	194	201	195	196	195
Bansei		206	202	202	197	204	199
Beeson 80		200	198	208	204	204	201
Mukden x Magna	F_1	196		202		199	
	F_2	199	199	205	197	202	198
Funman x Mukden	F_1	181		206		194	
	F_2	188	180+	199	186*+	194	183+
Bansei x Magna	F_1	203		202		203	
	F_2	201	201	200	200	200	201
Beeson 80 x Mukden	F_1	196		208		202	
	F_2	196	193	207	203	201	198
Beeson 80 x Funman	F_1	196		208		202	
	F_2	195	187	206	197	200	192+
Beeson 80 x Bansei	F_1	196		203		199	
	F_2	191*+	177*+	202+	196+	196+	186*+
		Geographic Origin					
Tastee	Parent	198	192	196	186	197	189
PI30.594		166	179	189	194	178	186
PI80.671		201	195	204	195	202	195
Richland		207	206	205	204	206	205
PI69.501		212	208	215	208	214	208
PI85.580		199	201	209	204	204	202
PI30.594 x PI69.501	F_1	191+		206+		198+	
	F_2	188+	175*+	202+	194+	195+	184*+
PI30.594 x Tastee	F_1	187+		198		193	
	F_2	191*	189	197	194	194*	191
PI69.501 x Richland	F_1	204+		210		208	
	F_2	204+	207	208	205	206+	206
PI80.671 x PI84.580	F_1	202		205		203	
	F_2	198	199	206	201	202	200
PI80.671 x Tastee	F_1	204		203		203	
	F_2	198	196	204	193	201	194
PI80.671 x Richland	F_1	198+		199		199+	
	F_2	199	198	202	198	200	198

Table A9. Mean seed yield (g m^{-2}) of parents, F_1 hybrids, and F_2 bulks of the four selection criteria of Maturity Group III grown in hill and row plot experiments conducted in 1990 and 1991

Entry	Generation	1990 Hill	1990 Row	1991 Hill	1991 Row	Combined Hill	Combined Row
		High Yield					
Zane	Parent	208	368	285	373	247	371
Resnik		208	395	264	405	236	400
A86-801024		274	437	327	429	301	433
Sherman		239	384	302	418	270	401
Resnik x Zane	F_1	238		334		286*	
	F_2	247	378	294	388	270	383
A86-801024 x Resnik	F_1	351*+		304		328*	
	F_2	253	418	323	372	288	395+
Sherman x A86-801024	F_1	303		275		289	
	F_2	280	443*	291	429	285	436
Sherman x Resnik	F_1	295*+		299		297*	
	F_2	274*	408	318	401	296*	405
Zane x Sherman	F_1	261		311		286	
	F_2	226	394	303	396	264	395
A86-801024 x Zane	F_1	277		332		304	
	F_2	246	414	314	418	282	416
		Restriction Fragment Length Polymorphism					
A81-356022	Parent	237	400	309	364	273	382
Illini		161	297	232	301	197	299
Dunfield		142	303	177	272	160	288
PI437.477B		98	223	206	253	152	238
PI437.477B x A81-356022	F_1	203		212+		208+	
	F_2	191	306+	256+	290	224+	298+
Illini x A81-356022	F_1	236		297		267	
	F_2	227	346+	295	334	261	340+
A81-356022 x Dunfield	F_1	270*		290*		280*	
	F_2	211	388	227+	332	219+	360
Dunfield x Illini	F_1	207*		251*		229*	
	F_2	216*	333	209	308	212	320*
PI437.477B x Illini	F_1	162		176+		169	
	F_2	121	279	174	269	147+	274
PI437.477B x Dunfield	F_1	144		210		177	
	F_2	146	283	198	254	172	268

* Significantly different from midparent value at the 0.05 probability level.
+ Significantly different from high-parent value at the 0.05 probability level.

Table A9. Continued

Entry	Generation	1990 Hill	1990 Row	1991 Hill	1991 Row	Combined Hill	Combined Row
		Isozyme					
Cloud	Parent	162	282	155	282	158	282
Cumberland		216	373	255	365	236	369
Will		245	342	281	357	263	350
Williams 82		245	371	291	324	268	347
Mandell		150	294	189	275	170	284
BSR 301		191	338	224	296	208	317
Shelby		213	322	272	284	242	303
Cumberland x Cloud	F_1	266*		303*		284*+	
	F_2	199	304+	233	329	216	317+
Will x Cloud	F_1	249		306*		277*	
	F_2	214	353*	242	327	228	340
BSR 301 x Cloud	F_1	257*+		221		239*	
	F_2	218	336	215	304	216*	320
Mandell x Shelby	F_1	192		254		223	
	F_2	182	306	240	303	211	305
Williams 82 x Cloud	F_1	261*		240+		250*	
	F_2	210	334	236+	311	223+	322
Mandell x Cloud	F_1	198		229*		214*+	
	F_2	170	282	207	283	189	283
		Geographic Origin					
PI80.470	Parent	64	176	42	74	53	125
PI104.708		100	265	206	270	153	268
PI61.940		150	286	160	244	155	265
PI82.235		130	233	160	217	145	225
Manchuria		130	311	190	328	160	320
PI54.592		168	284	184	240	176	262
PI104.708 x PI80.470	F_1	184*+		178*		181*	
	F_2	136*	268*	128+	204*+	132	236*
Manchuria x PI82.235	F_1	183*+		195		189*	
	F_2	139	249+	188	250+	164	249+
PI61.940 x PI54.592	F_1	219*+		235*		227*	
	F_2	173	312	196	304*+	185	308*+
PI54.592 x PI82.235	F_1	186		161		173	
	F_2	159	260	146	171*+	153	215+
PI61.940 x PI80.470	F_1	180*		119		150*	
	F_2	147	274*	124	173+	136	223+
PI82.235 x PI80.470	F_1	164*		172*		168*	
	F_2	122	240*	127	211*	125	226*

Table A10. Mean number of days to physiological maturity (days after 31 August) of parents, F_1 hybrids, and F_2 bulks of the four selection criteria of Maturity Group III grown in hill and row plot experiments conducted in 1990 and 1991

Entry	Generation	1990		1991		Combined	
		Hill	Row	Hill	Row	Hill	Row
		High Yield					
Zane	Parent	26	26	27	30	26	28
Resnik		27	28	29	30	28	29
A86-801024		28	28	28	30	28	29
Sherman		27	28	28	30	28	29
Resnik x Zane	F_1	26		29		28	
	F_2	27	28	29	30	28	29
A86-801024 x Resnik	F_1	28		28		28	
	F_2	27	28	29	29	28	29
Sherman x A86-801024	F_1	28		29		28	
	F_2	28	30*+	29	29	28	30
Sherman x Resnik	F_1	27		29		28	
	F_2	27	29	29	30	28	30
Zane x Sherman	F_1	27		28		28	
	F_2	27	27	28	29	27	28
A86-801024 x Zane	F_1	26		29*		28	
	F_2	26	28*	27	30	27	29
		Restriction Fragment Length Polymorphism					
A81-356022	Parent	29	31	30	31	30	31
Illini		28	32	29	30	28	31
Dunfield		21	23	22	23	22	23
PI437.477B		24	23	28	27	26	25
PI437.477B x A81-356022	F_1	26		29		28	
	F_2	28	29*	28+	30	28	30*
Illini x A81-356022	F_1	30		30		30	
	F_2	31*	35*+	30	32	30	34*+
A81-356022 x Dunfield	F_1	28*		29*		28*	
	F_2	29*	31*	30*	30*	30*	30*
Dunfield x Illini	F_1	26		28*		27	
	F_2	29*	30*	27	31*	28*	31*
PI437.477B x Illini	F_1	27		29		28	
	F_2	27	30*	30	30	28	30
PI437.477B x Dunfield	F_1	25		27*		26*	
	F_2	27*+	27*+	28*	29*	27*	28*+

* Significantly different from midparent value at the 0.05 probability level.
\+ Significantly different from high-parent value at the 0.05 probability level.

Table A10. Continued

Entry	Generation	1990 Hill	1990 Row	1991 Hill	1991 Row	Combined Hill	Combined Row
		Isozyme					
Cloud	Parent	26	30	28	28	27	29
Cumberland		28	28	30	30	29	29
Will		26	28	29	31	28	29
Williams 82		31	33	31	33	31	33
Mandell		22	24	26	26	24	25
BSR 301		28	28	30	30	29	29
Shelby		26	26	27	29	26	28
Cumberland x Cloud	F_1	27		29		28	
	F_2	28	31*	29	29	29	30
Will x Cloud	F_1	26		28		27	
	F_2	26	30	28	30	28	30
BSR 301 x Cloud	F_1	29*		31*		30*	
	F_2	29*	33*+	28	30*	29	32*+
Mandell x Shelby	F_1	24		26		25	
	F_2	24	26	26	28	25	27
Williams 82 x Cloud	F_1	30		30		30	
	F_2	29+	33	29+	32	29+	32
Mandell x Cloud	F_1	26*		26		26	
	F_2	27*	29*	28	30*+	27*	29*
		Geographic Origin					
PI80.470	Parent	29	31	33	37	31	34
PI104.708		28	30	27	28	27	29
PI61.940		24	26	25	24	25	25
PI82.235		27	28	31	30	29	29
Manchuria		24	27	28	28	26	28
PI54.592		28	32	29	29	29	31
PI104.708 x PI80.470	F_1	30		30+		30	
	F_2	28	32	32	32+	31	32
Manchuria x PI82.235	F_1	28		31		29	
	F_2	30*+	30*	29	32*+	30*	31*
PI61.940 x PI54.592	F_1	26		28		27	
	F_2	28	29	29	29*	28	29
PI54.592 x PI82.235	F_1	33*+		35*+		34*+	
	F_2	32*+	34*	31	31	32*+	32*
PI61.940 x PI80.470	F_1	31*		32		31*	
	F_2	32*+	33*	32	31+	33*	32*
PI82.235 x PI80.470	F_1	26+		30		28+	
	F_2	26+	28	31	30*+	28	29*

Table A11. Mean lodging score (from 1= all plants erect to 5= all plants prostrate) of parents, F_1 hybrids, and F_2 bulks of the four selection criteria of Maturity Group III grown in hill and row plot experiments conducted in 1990 and 1991

Entry	Generation	1990		1991		Combined	
		Hill	Row	Hill	Row	Hill	Row
		High Yield					
Zane	Parent	2.6	1.4	2.4	1.5	2.5	1.4
Resnik		2.0	1.2	2.1	1.4	2.1	1.3
A86-801024		2.0	1.5	1.8	1.6	1.9	1.6
Sherman		1.8	1.5	2.1	2.1	1.9	1.8
Resnik x Zane	F_1	2.0		2.0		2.0	
	F_2	2.1	1.2	2.1	1.6	2.1	1.4
A86-801024 x Resnik	F_1	2.2		1.8		2.0	
	F_2	2.0	1.4	1.9	1.6	1.9	1.5
Sherman x A86-801024	F_1	2.0		2.3		2.2	
	F_2	2.0	1.2	2.2	1.9	2.1	1.6
Sherman x Resnik	F_1	2.0		2.5		2.2	
	F_2	1.9	1.2	2.0	1.6	1.9	1.4+
Zane x Sherman	F_1	2.1		2.4		2.2	
	F_2	1.9	1.5	2.4	1.6	2.1	1.6
A86-801024 x Zane	F_1	2.2		2.4		2.3	
	F_2	2.2	1.6	2.3	1.9	2.3	1.8
	Restriction Fragment Length Polymorphism						
A81-356022	Parent	2.8	1.8	3.4	2.5	3.1	2.1
Illini		2.8	2.8	3.2	3.1	3.0	2.9
Dunfield		4.5	2.6	3.5	3.6	4.0	3.1
PI437.477B		3.9	1.4	3.5	2.4	3.7	1.9
PI437.477B x A81-356022	F_1	2.9+		2.8		2.8*+	
	F_2	2.8+	2.1	2.9	2.6	2.8*+	2.4
Illini x A81-356022	F_1	3.6*+		3.2		3.4	
	F_2	3.2	2.2	3.6	2.9	3.4	2.6
A81-356022 x Dunfield	F_1	3.2+		3.4		3.3+	
	F_2	3.4+	2.5	3.2	3.1	3.3+	2.8
Dunfield x Illini	F_1	3.2+		3.2		3.2+	
	F_2	3.8+	3.0	3.3	3.0	3.5	3.0
PI437.477B x Illini	F_1	3.0+		3.9		3.4	
	F_2	2.6*+	2.0	3.2	3.4	2.9+	2.7
PI437.477B x Dunfield	F_1	3.4*+		3.6		3.5	
	F_2	3.0*+	2.4	3.7	3.2	3.3*+	2.8

* Significantly different from midparent value at the 0.05 probability level.
\+ Significantly different from high-parent value at the 0.05 probability level.

Table A11. Continued

Entry	Generation	1990 Hill	1990 Row	1991 Hill	1991 Row	Combined Hill	Combined Row
		Isozyme					
Cloud	Parent	3.4	3.1	4.5	4.0	3.9	3.6
Cumberland		1.9	1.2	2.4	1.6	2.1	1.4
Will		1.9	1.5	2.5	2.0	2.2	1.8
Williams 82		1.9	1.5	2.0	1.6	1.9	1.6
Mandell		3.6	2.8	3.4	2.5	3.5	2.6
BSR 301		2.1	2.1	2.9	1.9	2.5	2.0
Shelby		2.0	2.0	2.2	2.2	2.1	2.1
Cumberland x Cloud	F_1	2.6		2.8+		2.7+	
	F_2	3.2	2.5	2.9+	3.5*	3.1+	3.0*+
Will x Cloud	F_1	2.5+		3.0+		2.8+	
	F_2	2.1+	2.0+	3.3+	3.0+	2.7+	2.5+
BSR 301 x Cloud	F_1	2.9		3.6+		3.2+	
	F_2	3.0	2.4+	2.8*+	3.0+	2.9+	2.7+
Mandell x Shelby	F_1	2.9		3.1		3.0	
	F_2	2.9	2.4	2.9	2.8	2.9+	2.6
Williams 82 x Cloud	F_1	3.2		3.4+		3.3+	
	F_2	3.0	2.1+	3.4+	2.8+	3.2+	2.4+
Mandell x Cloud	F_1	2.9		3.5+		3.2*+	
	F_2	2.9	2.5	3.3*+	3.5	3.1*+	3.0+
		Geographic Origin					
PI80.470	Parent	3.1	1.6	1.8	1.4	2.5	1.5
PI104.708		3.6	3.1	4.4	3.4	4.0	3.2
PI61.940		4.0	3.0	3.0	3.1	3.5	3.1
PI82.235		3.1	1.8	3.0	1.9	3.1	1.8
Manchuria		3.9	3.2	4.0	4.4	3.9	3.8
PI54.592		3.8	2.6	3.6	3.0	3.7	3.1
PI104.708 x PI80.470	F_1	3.4		4.1*		3.8	
	F_2	4.0*	2.5	3.1+	3.0*	3.7	2.8
Manchuria x PI82.235	F_1	3.9		4.2*		4.1*	
	F_2	3.9*	2.6	3.7	3.5+	3.9	3.1+
PI61.940 x PI54.592	F_1	3.6		2.9+		3.2	
	F_2	3.8	2.4	3.9*	3.9*	3.7	3.1
PI54.592 x PI82.235	F_1	4.1*		3.8		3.9*	
	F_2	3.2	2.5	3.4	3.1*	3.4	2.8
PI61.940 x PI80.470	F_1	4.1		4.2*+		4.2*+	
	F_2	3.6	2.9	4.2*+	3.4*	3.8*	3.1+
PI82.235 x PI80.470	F_1	2.9		2.2+		2.6	
	F_2	3.1	1.6	2.1+	1.5	2.4+	1.6

Table A12. Mean plant height (cm) of parents, F_1 hybrids, and F_2 bulks of the four selection criteria of Maturity Group III grown in hill and row plot experiments conducted in 1990 and 1991

Entry	Generation	1990		1991		Combined	
		Hill	Row	Hill	Row	Hill	Row
		High Yield					
Zane	Parent	78	90	95	102	86	96
Resnik		80	92	87	94	84	93
A86-801024		86	95	93	100	89	97
Sherman		79	82	93	96	86	89
Resnik x Zane	F_1	82		96		89	
	F_2	78	93	99	108*	89	101*
A86-801024 x Resnik	F_1	84		97		91	
	F_2	82	96	93	99	87	98
Sherman x A86-801024	F_1	85		83*+		84	
	F_2	84	98*	96	100	90	99*
Sherman x Resnik	F_1	85		87		86	
	F_2	85	92*	95	100	90	96*
Zane x Sherman	F_1	82		98		90	
	F_2	80	92*	99	102	89	97*
A86-801024 x Zane	F_1	86		98		92	
	F_2	84	102*	98	106	91	104*+
		Restriction Fragment Length Polymorphism					
A81-356022	Parent	93	108	108	124	100	116
Illini		94	99	108	114	101	107
Dunfield		78	96	108	106	93	101
PI437.477B		66	78	106	110	86	94
PI437.477B x A81-356022	F_1	86		103		95	
	F_2	81	98*+	108	112+	95	105+
Illini x A81-356022	F_1	86		110		98	
	F_2	85	104	118	124	102	114
A81-356022 x Dunfield	F_1	90		112		101	
	F_2	87	106	112	114	100	110
Dunfield x Illini	F_1	90		112		101	
	F_2	94	97	102	114	98	105
PI437.477B x Illini	F_1	88		98		93	
	F_2	84	98*	110	105	97	102
PI437.477B x Dunfield	F_1	83		108		96	
	F_2	86*	93*	102	110	94	102

* Significantly different from midparent value at the 0.05 probability level.
+ Significantly different from high-parent value at the 0.05 probability level.

Table A12. Continued

Entry	Generation	1990 Hill	1990 Row	1991 Hill	1991 Row	Combined Hill	Combined Row
		Isozyme					
Cloud	Parent	93	105	106	121	100	113
Cumberland		86	90	98	104	92	97
Will		82	96	83	98	82	97
Williams 82		87	101	107	109	97	105
Mandell		80	99	108	108	94	104
BSR 301		94	102	96	108	95	105
Shelby		87	98	98	109	92	104
Cumberland x Cloud	F_1	97*		108		102	
	F_2	84+	102	103	118	93	110*
Will x Cloud	F_1	96*		107*		101*	
	F_2	90	108*	98	116	94	112*
BSR 301 x Cloud	F_1	100		110		105*	
	F_2	88	103	112	116	100	110
Mandell x Shelby	F_1	82		108		95	
	F_2	84	98	110	109	97	104
Williams 82 x Cloud	F_1	97*		114		105	
	F_2	95	110*	116	116	106	113
Mandell x Cloud	F_1	98*		110		104	
	F_2	86	103	112	113	99	108
		Geographic Origin					
PI80.470	Parent	51	54	31	30	41	42
PI104.708		70	76	89	100	80	88
PI61.940		73	92	97	95	85	94
PI82.235		50	58	51	56	50	57
Manchuria		67	73	95	94	81	83
PI54.592		95	106	110	113	103	109
PI104.708 x PI80.470	F_1	83*+		95*		89*	
	F_2	74*	92*+	73	94*	76*	93*
Manchuria x PI82.235	F_1	66		84		75	
	F_2	62	83*	79	83*	72	83*
PI61.940 x PI54.592	F_1	92		98		95	
	F_2	86	102	104	111	97	106
PI54.592 x PI82.235	F_1	88*		100*		94	
	F_2	86*	99*	94	94*+	93*	97*+
PI61.940 x PI80.470	F_1	82*		110*		96*	
	F_2	77*	90*	87*	98*	83*	94*
PI82.235 x PI80.470	F_1	60		54		57	
	F_2	56	64	55	54*	55	59

Table A13. Mean number of days to flowering (days after June 30) of parents, F_1 hybrids, and F_2 bulks of the four selection criteria of Maturity Group III grown in hill and row plot experiments conducted in 1990 and 1991

Entry	Generation	1990		1991		Combined	
		Hill	Row	Hill	Row	Hill	Row
		High Yield					
Zane	Parent	24	24	17	19	20	21
Resnik		19	20	17	16	18	18
A86-801024		22	22	18	18	20	20
Sherman		21	21	18	18	19	19
Resnik x Zane	F_1	22		16		19	
	F_2	20+	21+	18	16+	19	19+
A86-801024 x Resnik	F_1	20		18		19	
	F_2	21	20	17	18	19	19
Sherman x A86-801024	F_1	26*+		19		22*+	
	F_2	20	23	17	18	18	21
Sherman x Resnik	F_1	21		18		20	
	F_2	20	20	17	18	18	19
Zane x Sherman	F_1	23		16		20	
	F_2	22	22	18	17+	20	19+
A86-801024 x Zane	F_1	21+		16		19	
	F_2	21+	23	16	18	19	20
		Restriction Fragment Length Polymorphism					
A81-356022	Parent	21	22	18	18	19	20
Illini		26	32	24	24	25	28
Dunfield		23	29	19	20	21	25
PI437.477B		26	28	19	18	22	23
PI437.477B x A81-356022	F_1	27*		20		23	
	F_2	25	23+	16	18	20	20+
Illini x A81-356022	F_1	30*		22		26*	
	F_2	28*	26+	20+	18*+	24	22+
A81-356022 x Dunfield	F_1	28*+		22*		25*+	
	F_2	22	26	21*	18+	22	22+
Dunfield x Illini	F_1	26		22		24	
	F_2	29*	28	20+	20*+	24	24*+
PI437.477B x Illini	F_1	34*+		25*		30*+	
	F_2	27	28	22	19*+	24	23+
PI437.477B x Dunfield	F_1	32*+		23*+		27*+	
	F_2	22	26	21	19+	22	22+

* Significantly different from midparent value at the 0.05 probability level.
+ Significantly different from high-parent value at the 0.05 probability level.

Table A13. Continued

Entry	Generation	1990 Hill	1990 Row	1991 Hill	1991 Row	Combined Hill	Combined Row
		Isozyme					
Cloud	Parent	28	29	22	22	25	26
Cumberland		26	28	18	19	22	24
Will		24	28	17	19	20	23
Williams 82		27	27	19	20	23	24
Mandell		21	21	17	18	19	20
BSR 301		25	26	18	19	22	22
Shelby		25	25	19	20	22	23
Cumberland x Cloud	F_1	28		20		24	
	F_2	27	29	19+	19*+	23	24
Will x Cloud	F_1	28		21		25	
	F_2	26	28	18+	18*+	22+	23
BSR 301 x Cloud	F_1	28		22		25	
	F_2	29	28	20	19+	24	24
Mandell x Shelby	F_1	26		18		22	
	F_2	22	22	18	18+	20	20
Williams 82 x Cloud	F_1	30		21		26	
	F_2	28	27	21	18*+	24	23+
Mandell x Cloud	F_1	26		19		22+	
	F_2	21+	22+	19+	18*+	20+	20+
		Geographic Origin					
PI80.470	Parent	32	31	26	25	29	28
PI104.708		26	26	19	20	23	24
PI61.940		20	21	20	18	20	19
PI82.235		32	33	23	24	28	28
Manchuria		27	28	21	22	24	25
PI54.592		33	38	30	26	32	32
PI104.708 x PI80.470	F_1	29		23+		26+	
	F_2	28	30	20+	23+	25+	26
Manchuria x PI82.235	F_1	32		25*		28	
	F_2	28	29+	21	20*+	23+	25+
PI61.940 x PI54.592	F_1	30		25+		28+	
	F_2	28	29+	22*+	21+	26+	25+
PI54.592 x PI82.235	F_1	39*		29*		34*	
	F_2	33	37	24*+	21*+	28+	29
PI61.940 x PI80.470	F_1	30		23+		27	
	F_2	32	24+	21*	20+	26	22+
PI82.235 x PI80.470	F_1	30		22*+		26	
	F_2	29	29	23*	22*+	26	26

Table A14. Mean seed weight (g 100^{-1} seeds) of parents, F_1 hybrids, and F_2 bulks of the four selection criteria of Maturity Group III grown in hill and row plot experiments conducted in 1990 and 1991

Entry	Generation	1990		1991		Combined	
		Hill	Row	Hill	Row	Hill	Row
		High Yield					
Zane	Parent	17	18	20	20	19	19
Resnik		14	15	15	15	15	15
A86-801024		17	16	19	18	18	17
Sherman		15	16	16	15	16	16
Resnik x Zane	F_1	16+		17+		16+	
	F_2	16*+	16	18+	17+	17+	17+
A86-801024 x Resnik	F_1	17*		20*		18*	
	F_2	16*	16	17+	16+	17+	16+
Sherman x A86-801024	F_1	17*		17+		17+	
	F_2	16+	17	18+	16+	17+	17
Sherman x Resnik	F_1	16*		16		16	
	F_2	15*	16	16	15	16	16
Zane x Sherman	F_1	17*		18+		18+	
	F_2	16+	17	18+	18+	17+	17+
A86-801024 x Zane	F_1	18*		18*+		18	
	F_2	18	18	20	19	19	19
		Restriction Fragment Length Polymorphism					
A81-356022	Parent	16	18	18	18	17	18
Illini		12	13	13	13	13	13
Dunfield		14	14	16	16	15	15
PI437.477B		13	13	15	14	14	14
PI437.477B x A81-356022	F_1	15+		17		16+	
	F_2	15*+	14+	16+	16+	16+	15+
Illini x A81-356022	F_1	14+		16+		15+	
	F_2	14+	15+	16+	15+	15+	15+
A81-356022 x Dunfield	F_1	17*		18		17*	
	F_2	16	16+	17	17	16+	17+
Dunfield x Illini	F_1	15		16		15*	
	F_2	14	14	16	15	15	14
PI437.477B x Illini	F_1	12		13*+		13*+	
	F_2	12	12	13*+	12*+	12*+	12*+
PI437.477B x Dunfield	F_1	14*+		15		15	
	F_2	13	14	15+	14*+	14*+	14+

* Significantly different from midparent value at the 0.05 probability level.
\+ Significantly different from high-parent value at the 0.05 probability level.

Table A14. Continued

Entry	Generation	1990 Hill	1990 Row	1991 Hill	1991 Row	Combined Hill	Combined Row
		Isozyme					
Cloud	Parent	14	14	16	15	15	14
Cumberland		16	17	18	18	17	17
Will		15	15	18	16	16	16
Williams 82		15	15	16	15	15	15
Mandell		15	16	18	17	16	16
BSR 301		16	16	18	16	17	16
Shelby		14	15	16	15	15	15
Cumberland x Cloud	F_1	16*		18		17*	
	F_2	16	16+	19*	16+	17*	16+
Will x Cloud	F_1	15		17		16	
	F_2	15	16	17	16	16	16
BSR 301 x Cloud	F_1	16*		16		16	
	F_2	16*	16	17	15	16	15
Mandell x Shelby	F_1	16*		18		17*	
	F_2	15	16	18	17	16	16
Williams 82 x Cloud	F_1	15		16		16	
	F_2	14	15	16	15	15	15
Mandell x Cloud	F_1	16*		17		16	
	F_2	15	15	17	16+	16	15+
		Geographic Origin					
PI80.470	Parent	15	16	16	16	16	16
PI104.708		18	20	22	21	20	20
PI61.940		16	17	17	17	16	17
PI82.235		20	19	20	20	20	20
Manchuria		12	13	14	13	13	13
PI54.592		12	12	13	12	13	12
PI104.708 x PI80.470	F_1	17		20+		18+	
	F_2	19*	18	19+	18+	19+	18+
Manchuria x PI82.235	F_1	15+		16+		16+	
	F_2	15+	14*	16+	14*+	16+	14*+
PI61.940 x PI54.592	F_1	14+		16		15+	
	F_2	14	14+	15+	14+	15+	14+
PI54.592 x PI82.235	F_1	17+		15*+		16+	
	F_2	15+	16+	16+	15*+	15+	15+
PI61.940 x PI80.470	F_1	16		15		15	
	F_2	16	16	17	16	16	16
PI82.235 x PI80.470	F_1	19*		21*		20*	
	F_2	18+	18	20*	19+	19*	18+

Table A15. Mean protein content (g kg^{-1}) of parents, F_1 hybrids, and F_2 bulks of the four selection criteria of Maturity Group III grown in hill and row plot experiments conducted in 1990 and 1991

Entry	Generation	1990		1991		Combined	
		Hill	Row	Hill	Row	Hill	Row
		High Yield					
Zane	Parent	416	409	373	386	395	398
Resnik		422	421	396	395	409	408
A86-801024		422	409	389	394	406	402
Sherman		413	414	378	385	395	399
Resnik x Zane	F_1	416		382+		399	
	F_2	419	419	392	390	406	404
A86-801024 x Resnik	F_1	423		387		405	
	F_2	416	412	391	397	404	404
Sherman x A86-801024	F_1	408		379+		394*+	
	F_2	415	411	384	386+	399+	398
Sherman x Resnik	F_1	416		386		401+	
	F_2	419	416	387	396	403	406
Zane x Sherman	F_1	414		387		400	
	F_2	416	411	377	384	396	398
A86-801024 x Zane	F_1	420		395		408*	
	F_2	425	412	385	390	405	401
		Restriction Fragment Length Polymorphism					
A81-356022	Parent	431	424	404	408	417	416
Illini		436	426	385	395	410	410
Dunfield		408	407	386	386	397	396
PI437.477B		462	464	418	434	440	449
PI437.477B x A81-356022	F_1	438		419		428+	
	F_2	444	448+	419*	421+	432	435+
Illini x A81-356022	F_1	432		388+		409	
	F_2	428	423	392+	401	409	412
A81-356022 x Dunfield	F_1	420		390+		405+	
	F_2	419	418	389+	397	404	407+
Dunfield x Illini	F_1	425		379		402	
	F_2	424	422	386	389	405	406
PI437.477B x Illini	F_1	450		414*		432	
	F_2	453	444+	419*	422+	436	434+
PI437.477B x Dunfield	F_1	446*+		401+		424+	
	F_2	446*+	439	406+	419+	426+	429*+

* Significantly different from midparent value at the 0.05 probability level.
\+ Significantly different from high-parent value at the 0.05 probability level.

Table A15. Continued

Entry	Generation	1990 Hill	1990 Row	1991 Hill	1991 Row	Combined Hill	Combined Row
		Isozyme					
Cloud	Parent	431	432	407	414	419	423
Cumberland		417	412	378	392	398	402
Will		426	419	392	400	409	409
Williams 82		421	418	392	402	407	410
Mandell		469	449	430	431	450	440
BSR 301		431	412	399	394	415	403
Shelby		419	419	385	392	402	406
Cumberland x Cloud	F_1	445*+		402*		424*	
	F_2	441*	434*	413*	419*	427*+	427*
Will x Cloud	F_1	442*		412*		427*+	
	F_2	438	432	405	420*	422*	426*
BSR 301 x Cloud	F_1	442*		414*		428*+	
	F_2	441	436*	410	417*	426*	426*
Mandell x Shelby	F_1	439+		404+		422+	
	F_2	436+	433+	403+	419*+	419*+	426+
Williams 82 x Cloud	F_1	443*		418*		430*+	
	F_2	440*	427	410*	416*	425*	422*
Mandell x Cloud	F_1	451+		415+		433+	
	F_2	449+	454*	419	438*	435+	446*
		Geographic Origin					
PI80.470	Parent	408	400	384	384	396	392
PI104.708		436	432	416	415	426	424
PI61.940		445	438	400	416	423	427
PI82.235		424	423	402	410	413	417
Manchuria		419	412	368	371	394	392
PI54.592		428	429	396	401	412	415
PI104.708 x PI80.470	F_1	417+		396+		407+	
	F_2	422+	412+	391*+	401+	406+	406+
Manchuria x PI82.235	F_1	418		394*		406	
	F_2	426	414	389+	408*	408	411
PI61.940 x PI54.592	F_1	445		406		425	
	F_2	437	434	405	404+	421	419
PI54.592 x PI82.235	F_1	432		408*		420	
	F_2	432	422	407+	419*	419	420
PI61.940 x PI80.470	F_1	419+		395		407+	
	F_2	420+	411+	401+	409*	410+	410+
PI82.235 x PI80.470	F_1	415		386+		401+	
	F_2	419	409+	390+	396+	405	403+

Table A16. Mean oil content (g kg^{-1}) of parents, F_1 hybrids, and F_2 bulks of the four selection criteria of Maturity Group III grown in hill and row plot experiments conducted in 1990 and 1991

Entry	Generation	1990 Hill	1990 Row	1991 Hill	1991 Row	Combined Hill	Combined Row
		High Yield					
Zane	Parent	215	218	226	225	220	221
Resnik		209	202	212	211	211	207
A86-801024		201	199	211	208	206	204
Sherman		215	209	225	215	219	212
Resnik x Zane	F_1	220		222		221*	
	F_2	214	208	219+	218	217	214+
A86-801024 x Resnik	F_1	204		214		209	
	F_2	210	204	214	210	212	207
Sherman x A86-801024	F_1	216		211*+		213+	
	F_2	208	209	213+	213	210+	211
Sherman x Resnik	F_1	214		219+		217	
	F_2	209	207	216+	208	213+	208
Zane x Sherman	F_1	219		223		221	
	F_2	212	210	225	225	219	218
A86-801024 x Zane	F_1	210		212*+		211+	
	F_2	203	208	216+	217	209+	212+
		Restriction Fragment Length Polymorphism					
A81-356022	Parent	192	193	198	199	195	196
Illini		186	186	199	196	192	191
Dunfield		209	199	210	210	209	205
PI437.477B		168	158	187	172	177	165
PI437.477B x A81-356022	F_1	192*		193		192	
	F_2	179+	164+	188	186+	184+	175+
Illini x A81-356022	F_1	188		202		195	
	F_2	189	184	199	193	194	188
A81-356022 x Dunfield	F_1	204		210		207	
	F_2	199	191	202	205	201+	198
Dunfield x Illini	F_1	201		212		206	
	F_2	199	189	204	204	202+	196
PI437.477B x Illini	F_1	173+		180*+		177*+	
	F_2	173+	163+	180*+	172*+	176*+	168*+
PI437.477B x Dunfield	F_1	183+		193+		188+	
	F_2	183+	180+	196+	182*+	189+	181+

* Significantly different from midparent value at the 0.05 probability level.
+ Significantly different from high-parent value at the 0.05 probability level.

Table A16. Continued

Entry	Generation	1990 Hill	1990 Row	1991 Hill	1991 Row	Combined Hill	Combined Row
		Isozyme					
Cloud	Parent	184	174	200	188	192	181
Cumberland		209	209	220	214	215	212
Will		202	200	218	210	210	205
Williams 82		208	197	204	199	206	198
Mandell		176	192	194	197	185	195
BSR 301		202	207	209	215	206	211
Shelby		208	199	210	216	209	208
Cumberland x Cloud	F_1	186+		204+		195*	
	F_2	184+	185+	192*+	192+	188*+	189+
Will x Cloud	F_1	187		192*+		189*+	
	F_2	185+	182+	192*+	182*+	188*+	182*+
BSR 301 x Cloud	F_1	183+		184*+		184*+	
	F_2	182+	174*+	189*+	187*+	185*+	180*+
Mandell x Shelby	F_1	198		209		204	
	F_2	199	194	202	208	201	201
Williams 82 x Cloud	F_1	186+		182*+		184*+	
	F_2	180*+	192	187*+	188	184*+	190
Mandell x Cloud	F_1	180		191		186	
	F_2	186	176+	191	178*+	189	177*+
		Geographic Origin					
PI80.470	Parent	204	202	203	208	203	206
PI104.708		194	187	197	195	195	191
PI61.940		196	195	212	204	204	199
PI82.235		204	194	198	204	201	199
Manchuria		199	198	212	212	206	205
PI54.592		197	177	195	188	196	183
PI104.708 x PI80.470	F_1	198		202		200	
	F_2	200	194	199	202+	199	198+
Manchuria x PI82.235	F_1	203		198+		200	
	F_2	195	178*+	203	192*+	199	185*+
PI61.940 x PI54.592	F_1	189		197+		194+	
	F_2	190	185+	199+	196+	195+	190+
PI54.592 x PI82.235	F_1	195		180*+		188*+	
	F_2	192+	182+	194	183*+	193	183*+
PI61.940 x PI80.470	F_1	196		186*+		191*+	
	F_2	191*+	188*+	197*+	186*+	194*+	187*+
PI82.235 x PI80.470	F_1	205		212*		209	
	F_2	202	195	206	204	204	199+

APPENDIX B. ANALYSES OF VARIANCE COMBINED OVER LOCATIONS AND ENVIRONMENTS

Table B1. Mean squares from the analysis of variance combined over locations for the traits measured in the hill plot experiment of Maturity Group II conducted in 1990 and 1991

Source of variation	df†	Traits							
		Yield		Maturity		Lodging		Height	
		1990	1991	1990	1991	1990	1991	1990	1991
		----- g m^{-2} ------		----- d -----		-- score --		------ cm -----	
Location (B)	1	209032.0*	1540.7	0.4	185.1	7.98	4.99	2134.4	2032.6*
Rep/B	2	2264.3*	4754.4*	10.4	14.4*	4.55*	0.57	252.9*	8.7
Entries (E) ‡	68	6336.2*	9586.8*	29.1*	25.6*	1.44*	1.21*	233.6*	394.3*
Among Criteria (C)	3	68414.3*	100054.0*	218.4*	203.5*	12.18*	13.81*	1733.5*	3126.5*
Within HY (E1)	15	3862.1*	4458.8*	7.4*	18.9*	0.41	0.42*	73.1	159.6*
Within RFLP (E2)	17	3607.3	5470.1*	10.1*	13.5*	0.94	0.37	88.1	195.9*
Within ISO (E3)	16	4019.8*	6520.5*	16.1*	13.5*	0.47	0.54	268.2*	447.9*
Within GO (E4)	17	1341.9*	4564.6*	44.4*	22.2*	1.94*	1.16*	218.4*	267.2*
B*E	68	1448.6*	1099.6	3.4*	3.8	0.36	0.27	44.8	43.9
B*C	3	924.4	1422.7	16.7	2.7	0.29	0.73	6.7	77.7
B*E1	15	2177.4	1788.1	0.9	3.1	0.42	0.14	68.5*	27.9
B*E2	17	2528.4*	731.3	3.2	3.8	0.49	0.25*	75.3*	68.3
B*E3	16	813.4	1428.1	2.0	4.3	0.36	0.32	18.3	33.0
B*E4	17	434.4	503.6	4.5*	4.2	0.19	0.28	24.9	38.8
Error	136	776.8	1038.2	2.4	3.9	0.41	0.23	34.7	60.8
R/BC	6	68013.2	92276.1	291.6	315.6	23.66	14.71	3055.6	4745.3
R/BE1	30	1111.4	1304.9	1.1	3.7	0.27	0.10	26.9	24.9
R/BE2	34	757.8	690.8	4.6	2.9	0.53	0.12	37.8	44.1
R/BE3	32	730.0	1192.8	1.7	3.9	0.37	0.35	27.7	55.9
R/BE4	34	583.6	923.9	1.6	5.6	0.40	0.28	46.7	115.6

* Significant at the 0.05 probability level.
† df= Degrees of freedom.
‡ HY= High yield; RFLP= Restriction fragment length polymorphism; ISO= Isozyme; GO= Geographic origin.

Table B1. Continued

Source of variation	df†	Traits							
		Flowering		Seed Weight		Protein		Oil	
		1990	1991	1990	1991	1990	1991	1990	1991
		----- d -----		--- g 100^{-1} ---		--- g kg^{-1} ---		--- g kg^{-1} ---	
Location (B)	1	9.9	41.5*	412.09*	1.42	15.26*	6.00	70.31*	0.38
Rep/B	2	4.1	18.7*	0.77	5.34	0.07	0.73	0.25	0.27
Entries (E) ‡	68	41.8*	28.4*	22.44*	23.98*	10.08*	8.11*	3.76*	2.52*
Among Criteria (C)	3	170.9*	236.4*	117.40*	183.63*	87.92*	97.01*	43.44*	39.70*
Within HY (E1)	15	20.4*	11.7*	2.40*	3.72*	0.58*	1.20	0.83*	0.36*
Within RFLP (E2)	17	30.0*	9.3*	5.31*	9.27*	2.03*	4.08*	1.13*	0.80*
Within ISO (E3)	16	39.5*	12.4*	45.89*	35.43*	10.40*	4.86*	1.50	0.45*
Within GO (E4)	17	51.9*	40.8*	18.30*	17.54*	12.53*	5.30*	4.09*	1.43*
B*E	68	5.4	3.3	1.27*	1.32*	0.62	0.51	0.47	0.18
B*C	3	0.9	4.0	8.49	2.60	1.18	0.82	0.72	0.76
B*E1	15	2.1	3.8	0.94	0.82	0.21	0.67	0.29	0.09
B*E2	17	3.6	3.0	0.44	1.07	0.38	0.21	0.30	0.13
B*E3	16	8.9*	3.8	1.46	1.95	0.62	0.55	0.70	0.15
B*E4	17	7.5	2.5	0.91	1.22	0.44	0.59*	0.28	0.22*
Error	136	4.4	2.5	0.69	0.92	0.47	0.38	0.41	0.16
R/BC	6	553.6	295.7	221.08	214.43	89.51	56.58	46.40	13.59
R/BE1	30	3.2	2.7	0.54	0.54	0.37	0.34	0.65	0.13
R/BE2	34	4.3	2.2	0.47	0.78	0.62	0.41	0.98	0.21
R/BE3	32	3.7	2.2	1.03	1.31	1.04	0.49	1.36	0.19
R/BE4	34	6.1	3.0	0.62	1.13	0.53	0.27	0.70	0.11

Table B2. Mean squares from the analysis of variance combined over locations for the traits measured in the row plot experiment of Maturity Group II conducted in 1990 and 1991

Source of variation	df†	Traits							
		Yield		Maturity		Lodging		Height	
		1990	1991	1990	1991	1990	1991	1990	1991
		----- g m^{-2} ------		----- d -----		---- score ----		----- cm -------	
Location (B)	1	60969.5*	35215.6*	28.0	5.0	26.07*	6.23*	8201.2*	2040.2*
Rep/B	2	252.8	170.5	1.9	15.4	0.27	0.24	135.1	10.8
Entries (E) ‡	44	11695.6*	16572.1*	49.2*	45.5*	1.13*	1.36*	308.8*	602.9*
Among Criteria (C)	3	126344.9*	164299.8*	222.2*	234.9*	7.36	7.23*	1295.8*	2242.1*
Within HY (E1)	9	1712.5	4202.8*	11.5*	51.0*	0.16*	0.32	85.0*	103.5
Within RFLP (E2)	11	3737.9	2678.1*	23.6*	26.6	0.29	0.59*	126.8*	241.0*
Within ISO (E3)	10	3033.0*	6053.4*	41.6*	18.3*	0.40	0.93*	309.4*	706.9*
Within GO (E4)	11	2519.2*	8723.6*	61.8*	21.9	1.78*	1.79*	389.5*	823.4*
B*E	44	1317.6*	981.4	3.4*	9.6	0.32*	0.23	34.7	46.5*
B*C	3	8499.7	148.9	3.6	23.0	1.54	0.64	51.6	57.6
B*E1	9	638.1*	1260.9	3.1*	7.7	0.03	0.13	23.4	65.7
B*E2	11	1467.3	893.4	4.7*	12.1	0.34	0.17	16.3	53.9*
B*E3	10	557.2	940.0	3.8	5.0	0.16*	0.16	32.4	20.9
B*E4	11	544.2*	1106.5	1.9	9.4*	0.29*	0.32	61.2	43.5*
Error	88	439.1	1093.5	1.9	6.3	0.10	0.19	27.4	26.6
R/BC	6	31109.4	60459.2	292.2	357.1	7.69	10.58	2222.9	3986.6
R/BE1	18	250.7	1186.9	0.8	14.9	0.09	0.11	13.7	30.1
R/BE2	22	857.1	876.8	1.8	6.3	0.16	0.17	24.9	20.3
R/BE3	20	449.7	1604.8	1.9	4.8	0.07	0.33	20.8	43.6
R/BE4	22	238.1	624.8	3.1	3.9	0.10	0.15	41.6	14.7

* Significant at the 0.05 probability level.
† df= Degrees of freedom.
‡ HY= High yield; RFLP= Restriction fragment length polymorphism; ISO= Isozyme; GO= Geographic origin.

Table B2. Continued

Source of variation	df†	Traits							
		Flowering		Seed Weight		Protein		Oil	
		1990	1991	1990	1991	1990	1991	1990	1991
		----- d -----		---- g 100^{-1} --		--- g kg^{-1} ---		- g kg^{-1} ---	
Location (B)	1	158.7*	0.4	213.97*	28.74*	1.44	28.56*	7.20	6.80
Rep/B	2	2.9	0.1	0.34	0.56	0.65	1.05	1.00	0.29
Entries (E) ‡	44	38.3*	12.1*	28.08*	19.87*	9.67*	8.26*	3.74*	2.58*
Among Criteria (C)	3	156.8*	66.9*	82.44*	80.60*	41.65*	61.61*	22.59*	22.89*
Within HY (E1)	9	17.1*	7.1*	2.82*	6.16*	1.05	1.58	0.14	0.43
Within RFLP (E2)	11	18.5*	0.7	6.98*	3.69	1.85*	4.12*	1.16*	1.15*
Within ISO (E3)	10	13.9*	5.1	72.54*	40.93*	12.46*	7.67*	3.32*	0.92*
Within GO (E4)	11	64.9*	18.9*	15.08*	11.39*	12.69*	3.93*	4.35*	1.63*
B*E	44	3.8	1.9*	0.93*	1.75	0.31	0.47	0.34	0.24
B*C	3	8.9	0.9	4.31	0.83	0.12	0.59	0.21	0.17
B*E1	9	2.0	1.1	0.29	0.61	0.33	0.57	0.17	0.29
B*E2	11	1.9	1.1	0.47	2.18	0.36	0.47	0.38	0.16
B*E3	10	3.5	4.1*	0.69	2.53	0.63	0.32	0.72	0.20
B*E4	11	6.2*	2.0	1.22*	1.82	0.53	0.50	0.22	0.34*
Error	88	2.8	1.3	0.51	1.34	0.36	0.52	0.38	0.27
R/BC	6	266.4	88.2	177.76	137.17	56.94	40.69	25.23	12.94
R/BE1	18	1.6	1.3	0.39	1.28	0.24	0.57	0.52	0.25
R/BE2	22	2.0	1.5	0.33	1.32	0.25	0.40	0.41	0.30
R/BE3	20	6.0	0.7	0.78	1.91	0.47	0.38	0.38	0.38
R/BE4	22	1.7	1.5	0.51	1.04	0.29	0.76	0.50	0.15

Table B3. Mean squares from the analysis of variance combined over locations for the traits measured in the hill plot experiment of Maturity Group III conducted in 1990 and 1991

Source of variation	df†	Traits							
		Yield		Maturity		Lodging		Height	
		1990	1991	1990	1991	1990	1991	1990	1991
		------ g m^{-2} ------		----- d ----		--- score ---		------ cm -------	
Location (B)	1	173142.1*	27838.1	0.3	9.4	3.29	2.19	2365.4	1084.1*
Rep/B	2	696.1	2730.4	1.1	23.2*	0.39	0.74	292.5*	27.3
Entries (E) ‡	68	12145.2*	15894.2*	18.9	14.1*	2.09*	2.02*	454.9*	997.5*
Among Criteria (C)	3	136714.7*	227103.2*	43.2	53.0*	30.11*	21.46*	3157.3*	8834.5*
Within HY (E1)	15	5400.7*	1594.1	1.7	1.5	0.17	0.18	30.9	87.5
Within RFLP (E2)	15	9300.2*	8317.2*	24.2*	15.6*	1.02*	0.31	181.4*	92.8
Within ISO (E3)	18	4697.1*	5838.5*	19.2*	10.9*	1.22*	1.28*	152.9*	257.5*
Within GO (E4)	17	5201.9*	7532.8*	31.0*	21.0*	0.90*	2.48*	856.4*	2008.8*
B*E	68	1780.6*	1632.1	1.9	2.8*	0.16	0.24	41.3	90.8
B*C	3	10702.8	3807.6	9.8	2.7	0.25	0.38	26.9	58.4
B*E1	15	1311.3	2177.2	1.0	0.7	0.26	0.22	43.5	38.2
B*E2	15	1607.9	1245.8	3.1	2.4	0.20	0.29	70.9	97.2
B*E3	18	1590.4*	1186.3	1.5	1.6	0.28	0.26	27.5	75.9
B*E4	17	858.1	1528.5	2.9	6.3*	0.25	0.14	66.1	155.5
Error	136	962.9	1578.1	1.4	1.7	0.29	0.30	30.6	81.4
R/BC	6	101908.0	115854.8	279.1	203.8	19.78	21.50	4858.9	9767.6
R/BE1	30	1299.3	935.0	0.9	1.2	0.17	0.07	28.8	20.1
R/BE2	30	1257.9	541.4	2.3	3.7	0.53	0.06	46.7	79.0
R/BE3	36	724.6	838.4	2.9	0.9	0.32	0.14	41.3	14.4
R/BE4	34	667.3	652.7	1.8	2.2	0.36	0.14	41.6	50.9

* Significant at the 0.05 probability level.
† df= Degrees of freedom.
‡ HY= High yield; RFLP= Restriction fragment length polymorphism; ISO= Isozyme; GO= Geographic origin.

Table B3. Continued

Source of variation	df†	Traits							
		Flowering		Seed Weight		Protein		Oil	
		1990	1991	1990	1991	1990	1991	1990	1991
		----- d -----		--- g 100^{-1} -----		--- g kg^{-1} ---		---- g kg^{-1} ---	
Location (B)	1	98.0	9.1	279.09*	12.44	0.005	0.53	3.41	7.94
Rep/B	2	21.5*	36.9*	9.86*	3.16*	2.46*	2.11*	0.27	2.06
Entries (E) ‡	68	69.5*	35.9*	10.35*	14.61*	7.39*	7.28*	6.07*	5.78*
Among Criteria (C)	3	827.2*	412.6*	53.15*	55.03*	60.77*	50.82*	67.30*	60.67*
Within HY (E1)	15	11.4*	2.7	4.41*	9.41*	0.74	1.69*	1.21	1.15*
Within RFLP (E2)	15	51.8*	22.1*	8.37*	10.91*	8.48*	8.24*	5.72*	3.86*
Within ISO (E3)	18	25.6*	11.0*	2.05*	2.89	6.12*	6.46*	4.79*	4.99*
Within GO (E4)	17	57.6*	35.8*	18.89*	27.31*	4.25*	4.84*	1.01*	2.79*
B*E	68	7.9	3.6	0.54	1.09	0.76	0.51	0.82	0.60
B*C	3	13.6	4.6	0.06	1.38	0.84	1.55	0.88	0.96
B*E1	15	3.2	2.8	0.27	0.48	0.38	0.44	0.52	0.15
B*E2	15	7.9	4.4	0.32	0.69	0.64	0.44	0.54	0.81
B*E3	18	8.0	3.8	0.58	1.39	0.73	0.57	1.25	0.73
B*E4	17	20.7*	3.3	1.20	1.62*	0.62	0.36	0.43	0.61
Error	136	6.8	3.5	0.54	0.76	0.60	0.61	0.77	0.44
R/BC	6	703.6	314.2	113.96	168.78	74.34	76.68	60.94	51.68
R/BE1	30	6.9	1.3	0.63	0.79	0.30	0.33	0.44	0.25
R/BE2	30	12.8	1.3	0.73	0.76	0.64	1.18	0.97	0.95
R/BE3	36	5.7	0.6	0.88	0.70	0.87	0.62	1.06	0.94
R/BE4	34	9.5	5.3	0.63	0.67	0.71	0.44	0.87	0.45

Table B4. Mean squares from the analysis of variance combined over locations for the traits measured in the row plot experiment of Maturity Group III conducted in 1990 and 1991

Source of variation	df†	Traits							
		Yield		Maturity		Lodging		Height	
		1990	1991	1990	1991	1990	1991	1990	1991
		----- g m^{-2} ------		----- d -----		--- score ---		----- cm ------	
Location (B)	1	46403.4	40356.6	222.2*	2.4	6.23*	0.31	1736.0	350.0
Rep/B	2	3036.2*	9893.6*	2.3	27.6*	0.07	0.09	118.7*	97.6
Entries (E) ‡	44	15073.4*	22901.5*	30.3*	19.8*	1.49*	2.73*	644.1*	1254.9*
Among Criteria (C)	3	140529.2*	232559.1*	26.2	5.5	9.37*	15.43*	3358.4*	7727.5*
Within HY (E1)	9	2425.4*	1757.8	5.6*	0.8	0.08	0.18	114.7*	79.9*
Within RFLP (E2)	9	11178.6*	5592.1*	58.6*	29.4*	0.94*	0.63	293.6*	159.5*
Within ISO (E3)	12	3741.2*	3254.1*	34.4*	13.2*	1.12*	2.28*	103.5*	166.8*
Within GO (E4)	11	5444.5*	17926.0*	25.2*	38.9*	1.26*	3.50*	1215.0*	2545.9*
B*E	44	689.6*	898.9*	2.5*	2.0	0.24*	0.16*	39.3	34.6
B*C	3	2273.4	2400.9*	6.3	4.8	0.69	0.16	227.8*	7.3
B*E1	9	322.9	1555.6	0.8	1.5	0.08	0.12	11.8	21.8
B*E2	9	901.8*	439.3	2.3	3.7	0.16	0.32*	14.3	44.8
B*E3	12	551.0	758.9	1.2	1.1	0.23	0.13	19.9	41.9*
B*E4	11	570.1	527.8	4.8*	1.3	0.33	0.09	48.9*	37.6
Error	88	329.0	828.9	1.2	1.9	0.13	0.10	20.1	40.6
R/BC	6	46680.4	68032.4	241.9	183.9	9.38	14.76	3510.7	1551.2
R/BE1	18	393.0	1374.9	1.2	0.8	0.04	0.15	18.7	31.7
R/BE2	18	278.4	2783.5	1.3	2.2	0.08	0.19	31.2	91.8
R/BE3	24	268.8	1262.4	1.2	1.1	0.14	0.34	16.9	95.7
R/BE4	22	331.5	1180.1	1.0	2.4	0.20	0.52	20.2	88.9

* Significant at the 0.05 probability level.
† df= Degrees of freedom.
‡ HY= High yield; RFLP= Restriction fragment length polymorphism; ISO= Isozyme; GO= Geographic origin.

Table B4. Continued

Source of variation	df†	Traits							
		Flowering		Seed Weight		Protein		Oil	
		1990	1991	1990	1991	1990	1991	1990	1991
		------ d -----		---- g 100^{-1} ---		---- g kg^{-1} ----		-- g kg^{-1} ---	
Location (B)	1	154.9	2.2	199.65*	1.12	1.68	12.53*	25.60	0.92
Rep/B	2	10.8	2.6	0.86	0.21	0.13	0.66	2.31*	0.63
Entries (E) ‡	44	70.9*	19.4*	11.56*	15.36*	7.74*	9.18*	7.42*	7.34*
Among Criteria (C)	3	455.4*	139.4*	35.24*	27.88*	29.74*	38.85*	47.68*	38.93*
Within HY (E1)	9	7.8*	2.1	3.99*	11.34*	0.61	0.93*	0.96	1.58*
Within RFLP (E2)	9	32.6*	11.9*	9.86*	10.35*	11.57*	10.66*	7.92*	7.33*
Within ISO (E3)	12	28.6*	5.6*	1.95	3.07*	6.71*	8.56*	5.64*	7.04*
Within GO (E4)	11	93.2*	21.1*	22.62*	32.27*	5.51*	7.66*	2.53*	3.44*
B*E	44	6.2*	1.4	1.16*	0.59	0.41	0.43	0.48	0.44
B*C	3	9.7	2.0	2.98*	0.77	0.07	1.00	0.01	0.74
B*E1	9	2.0	0.7	0.69	0.59	0.30	0.17	0.82	0.36
B*E2	9	5.5*	0.9	0.34	0.68	0.37	0.54	1.09*	0.22
B*E3	12	9.8*	1.6*	1.01*	0.44	0.31	0.33	0.59	0.87
B*E4	11	5.2	1.9	1.78*	0.68	0.36	0.48	0.36	0.16
Error	88	3.9	2.1	0.37	0.76	0.31	0.60	0.48	0.72
R/BC	6	387.7	110.2	78.38	113.08	49.38	59.98	44.52	47.32
R/BE1	18	2.3	3.0	0.32	0.49	0.30	0.32	0.75	0.19
R/BE2	18	2.0	4.8	0.34	0.79	0.45	0.65	0.42	0.45
R/BE3	24	4.2	3.5	0.36	1.41	0.39	0.67	1.05	0.66
R/BE4	22	5.4	3.0	0.50	0.72	0.29	0.61	0.65	0.47

Table B5. Mean squares from the analysis of variance combined over environments for the traits measured in the hill plot experiment of Maturity Group II

Source of variation	df†	Traits							
		Yield	Maturity	Lodging	Height	Flowering	Seed Weight	Protein	Oil
		g m^{-2}	d	score	cm	d	g 100^{-1}	---- g kg^{-1} ----	
Environment (A)	3	162710.2*	77.8	5.57	10611.4*	712.3*	632.89*	239.81*	20.64*
Rep/A	4	3509.2*	12.8*	2.56*	132.4*	11.1*	3.04*	1.05	0.67
Entries (E) ‡	68	13613.8*	47.6*	2.23*	572.1*	64.4*	44.40*	17.05*	5.62*
Among Criteria (C)	3	163428.8*	433.9*	24.56*	4665.2*	397.1*	291.53*	185.36*	83.65*
Within HY (E1)	15	6065.3*	16.0*	0.41	204.9*	28.8*	5.32*	1.06*	0.78*
Within RFLP (E2)	17	7128.2*	19.7*	0.81*	221.4*	30.3*	13.74*	4.93*	1.56*
Within ISO (E3)	16	8767.5*	23.0*	0.77*	650.3*	45.3*	78.95*	14.03*	0.83
Within GO (E4)	17	4882.9*	58.5*	2.67*	450.9*	89.1*	33.54*	16.42*	4.68*
A*E	204	1619.1*	4.5*	0.35	48.0	5.0	1.52*	0.70*	0.42
A*C	9	5650.8	8.8	0.68	99.1	4.8	7.75	1.07	0.55
A*E1	45	2073.5*	4.4*	0.33*	41.3*	3.1	0.85*	0.53	0.26
A*E2	51	1736.4*	3.4	0.41	68.7*	5.4	0.77	0.59	0.27
A*E3	48	1338.0	4.0	0.31	39.0	6.9*	1.91*	0.80	0.66
A*E4	51	653.7	5.5	0.30	32.7	4.5	1.49*	0.81*	0.44
Error	272	907.5	3.2	0.32	47.8	3.4	0.81	0.51*	0.55
R/AC	12	80143.3	303.6	19.19	3900.4	424.7	217.03	73.04	29.99
R/AE1	60	1208.1	2.3	0.19	25.9	2.9	0.54	0.36	0.39
R/AE2	68	724.3	3.7	0.33	40.8	3.3	0.63	0.51	0.59
R/AE3	64	961.4	2.9	0.36	41.9	2.9	1.17	0.76	0.77
R/AE4	68	753.8	3.6	0.34	81.2	4.6	0.88	0.40	0.41

* Significant at the 0.05 probability level.
† df= Degrees of freedom.
‡ HY= High yield; RFLP= Restriction fragment length polymorphism; ISO= Isozyme; GO= Geographic origin.

Table B6. Mean squares from the analysis of variance combined over environments for the traits measured in the row plot experiment of Maturity Group II

Source of variation	df†	Traits							
		Yield	Maturity	Lodging	Height	Flowering	Seed Weight	Protein	Oil
		g m^{-2}	d	score	cm	d	g 100^{-1}	--- g kg^{-1} ---	
Environment (A)	3	34496.6*	36.2	13.88*	4544.4*	264.6*	158.49*	47.84*	7.88*
Rep/A	4	211.7	8.9	0.25	72.9*	1.5	0.45	0.54	0.19
Entries (E) ‡	44	25738.6*	78.3*	2.12*	842.9*	43.3*	44.97*	16.69*	5.57*
Among Criteria (C)	3	294001.2*	463.9*	13.40*	3495.4*	215.8*	155.60*	103.94*	46.03*
Within HY (E1)	9	3264.1	47.2*	0.28*	172.0*	21.6*	6.86*	1.82*	0.28
Within RFLP (E2)	11	5449.5*	43.0*	0.49	333.4*	9.0	9.04	5.19*	1.74*
Within ISO (E3)	10	6884.4*	40.6*	0.68	928.1*	15.6*	109.08*	18.93*	3.08*
Within GO (E4)	11	8393.6*	68.3*	3.47*	1099.8*	73.6*	23.62*	14.53*	4.99*
A*E	132	1609.4*	8.9*	0.30*	49.9*	4.3*	1.88*	0.72*	0.45
A*C	9	5375.9	14.7	1.05	77.7	6.6	3.78	0.65	0.26
A*E1	27	1517.0*	8.8	0.12	35.2	1.9	1.00	0.57	0.25
A*E2	33	1109.5	7.8*	0.29*	34.9	4.3*	1.43*	0.53	0.37
A*E3	30	1233.2	9.0*	0.33	46.8	3.7	2.54*	0.72	0.69*
A*E4	33	1499.8*	8.7*	0.23*	72.6*	6.2*	1.96*	1.04*	0.52
Error	176	766.4	4.5	0.15	26.9	2.0	0.92	0.42	0.37
R/AC	12	45787.5	324.7	9.14	3104.8	177.3	157.46	48.82	19.08
R/AE1	36	719.1	7.9	0.10	21.9	1.4	0.83	0.41	0.38
R/AE2	44	867.2	4.1	0.16	22.6	1.8	0.83	0.32	0.36
R/AE3	40	1027.4	3.4	0.19	32.2	3.3	1.35	0.43	0.38
R/AE4	44	431.4	3.5	0.13	28.1	1.6	0.78	0.52	0.33

* Significant at the 0.05 probability level.
† df= Degrees of freedom.
‡ HY= High yield; RFLP= Restriction fragment length polymorphism; ISO= Isozyme; GO= Geographic origin.

Table B7. Mean squares from the analysis of variance combined over environments for the traits measured in the hill plot experiment of Maturity Group III

Source of variation	df†	Traits							
		Yield	Maturity	Lodging	Height	Flowering	Seed Weight	Protein	Oil
		g m^{-2}	d	score	cm	d	g 100^{-1}	--- g kg^{-1} ----	
Environment (A)	3	112759.4*	97.5*	2.69	10988.9*	1640.4*	193.40*	477.83*	19.68*
Rep/A	4	1713.2	12.4*	0.49	185.5*	27.7*	5.52*	2.47*	1.89*
Entries (E) ‡	68	25468.7*	30.2*	3.65*	1229.1*	96.3*	23.21*	13.51*	10.98*
Among Criteria (C)	3	367622.7*	89.0*	50.24*	10872.4*	1206.0*	107.11*	107.18*	125.95*
Within HY (E1)	15	3974.0	2.1*	0.21	49.7	8.6*	11.74*	1.79*	1.89*
Within RFLP (E2)	15	15797.8*	35.4*	0.82*	133.6	57.5*	18.51*	14.98*	9.08*
Within ISO (E3)	18	9055.6*	27.6*	2.15*	275.5*	31.2*	3.84*	12.09*	8.96*
Within GO (E4)	17	9966.3*	42.9*	2.54*	2544.5*	81.1*	43.17*	7.49*	2.52*
A*E	204	1994.5*	3.2*	0.34	116.5*	8.6*	1.19*	0.76	0.73
A*C	9	8320.6	4.8	0.80	374.1	25.1	2.18	1.58	1.53
A*E1	45	2169.8*	0.9	0.21	50.1*	3.9	0.94*	0.49	0.38
A*E2	45	1557.6	3.5	0.34	102.9	9.6	0.59	0.94	0.61
A*E3	54	1419.0	1.9	0.29	79.4	5.8	1.03	0.59	0.94
A*E4	51	1718.5*	5.9*	0.42	180.7*	12.1	1.95*	0.86	0.77
Error	272	1270.5	1.9	0.32	60.3	6.0*	0.79	0.62	0.63
R/AC	12	108882.1	241.4	20.64	7313.3	508.9	141.38	75.52	56.30
R/AE1	60	1307.1	0.8	0.16	30.2	4.9	0.56	0.31	0.31
R/AE2	60	2020.7	2.2	0.37	69.3	8.8	0.76	0.64	0.71
R/AE3	72	993.5	1.9	0.33	68.5	4.6	1.15	0.77	0.86
R/AE4	68	923.8	2.1	0.44	65.3	6.3	0.67	0.66	0.67

* Significant at the 0.05 probability level.
† df= Degrees of freedom.
‡ HY= High yield; RFLP= Restriction fragment length polymorphism; ISO= Isozyme; GO= Geographic origin.

Table B8. Mean squares from the analysis of variance combined over environments for the traits measured in the row plot experiment of Maturity Group III

Source of variation	df†	Traits							
		Yield	Maturity	Lodging	Height	Flowering	Seed Weight	Protein	Oil
		g m^{-2}	d	score	cm	d	g 100^{-1}	--- g kg^{-1} ---	
Environment (A)	3	27884.7	85.8	9.68*	2983.5*	1365.8*	72.42*	123.40*	21.61*
Rep/A	4	6464.8*	14.7*	0.08	107.9*	6.7	0.53	0.75	0.63
Entries (E) ‡	44	36041.6*	41.1*	3.87*	1735.6*	75.1*	26.00*	15.67*	14.23*
Among Criteria (C)	3	374767.9*	15.9	24.80*	10458.7*	547.7*	66.74*	64.02*	89.66*
Within HY (E1)	9	3341.0*	3.4	0.18	145.3*	6.9*	13.62*	1.05*	2.27*
Within RFLP (E2)	9	15665.7*	80.3*	1.28*	348.1*	36.9*	19.43*	21.64*	14.67*
Within ISO (E3)	12	6001.2*	38.9*	3.02*	234.4*	23.0*	4.55*	14.92*	11.96*
Within GO (E4)	11	19859.1*	48.9*	4.22*	3430.7*	89.9*	53.80*	10.37*	5.55*
A*E	132	1174.1*	4.3*	0.25*	79.1*	7.6*	0.89*	0.67*	0.54
A*C	9	3346.9	5.6	0.49	276.6	23.6	1.40	1.54	0.52
A*E1	27	906.4	1.7	0.09	26.7	1.9	0.99	0.32	0.49
A*E2	27	815.8*	4.4	0.26*	54.7	4.7*	0.59	0.49	0.63
A*E3	36	768.2	3.3*	0.25*	32.6*	7.5*	0.64	0.33	0.73
A*E4	33	1536.2*	6.9*	0.32*	138.9*	10.5*	1.18*	1.22*	0.31
Error	176	578.9	1.6	0.11	30.4	3.0	0.57	0.48	0.72
R/AC	12	57356.8	212.9	12.08	4857.8	248.9	95.74	54.68	45.92
R/AE1	36	663.9	1.2	0.06	19.4	1.8	0.56	0.32	0.50
R/AE2	36	409.8	2.6	0.07	55.1	1.6	0.55	0.81	0.68
R/AE3	48	553.6	1.2	0.14	15.7	2.4	0.53	0.50	0.99
R/AE4	44	492.3	1.5	0.17	35.5	5.4	0.58	0.37	0.55

* Significant at the 0.05 probability level.
† df= Degrees of freedom.
‡ HY= High yield; RFLP= Restriction fragment length polymorphism; ISO= Isozyme; GO= Geographic origin.